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RA Raha S.S., Loquellano N.A., McKernan P.J., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hate S., Garcia A.M., Gay L.O., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RN Proc. Natl. Acad. Sci. U.S.A. 99:16699-16903(2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. Metallothionien-TGF alpha model.
RC 10 month old virgin mouse. Taken by biopsy.;
RG NIH MGC Project;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
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CC -----
EMBL: BC051033; AAH51033.1; -: mRNA.
DR Ensembl: ENSMUSG0000057092; Mus musculus.
DR MGI: MGI:107497; Fxyd3.
DR GO: GO:0005615; C:extracellular space; RCA.
DR GO: GO:0016021; C:integral to membrane; RCA.
DR InterPro: IPR000272; FXYD.
DR Pfam: PF02038; ATP1G1_PLM MAT8; 1.
DR PROSITE: PS01310; FXYD; 1.
SQ SEQUENCE 70 AA; 7773 MW; AB2A5EAF1490BF08 CRC64;

Query Match 44.0%; Score 203; DB 2; Length 70;
Best Local Similarity 59.4%; Pred. No. 8e-14;
Matches 41; Conservative 10; Mismatches 16; Indels 2; Gaps 2;

QY 1 MERVTLALL-LLAGLTALEANDPFANKDDPFYDWNQLQSLGICGGLLAIAAGIAVLGSK 59
DB 1 MQEVLISLLVLLAGLTLDANDP-ENKNDPFYDWSLRVGGILCAGILCALGIIVLMG 59

QY 60 KCKYSSQK 68
DB 60 KCKKFRQK 68

RESULT 13
Q3SZX0_BOVIN PRELIMINARY; PRT; 92 AA.
AC Q3SZX0;
DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2005, sequence version 1.
DT 07-MAR-2006, entry version 4.
DE Hypothetical protein.
OS Bos taurus [Bovine].
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=Crossbred x Angus; TISSUE=Liver;
RA Moore S., Alexander L., Brownstein M., Guan L., Lobo S., Meng Y.,
RA Tanaguchi M., Wang Z., Yu J., Prange C., Schreiber K., Shennen C.,
RA Wagner L., Balu M., Barbasuk S., Barber S., Babakiaff R., Beland J.,
RA Chun E., Del Rio L., Gibson S., Hanson R., Kirkpatrick R., Liu J.,
RA Matsuo C., Mayo M., Santos R.R., Stott J., Tsai M., Wong D.,
RA Siddiqui A., Holt R., Jones S.J., Marra M.A.;
RL Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
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DR EMBL: BC102671; AAI02672.1; -: mRNA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005216; F:ion channel activity; IEA.
DR GO: GO:0006811; F:ion transport; IEA.
DR InterPro: IPR000272; FXYD.
DR Pfam: PF02038; ATP1G1_PLM MAT8; 1.
DR PROSITE: PS01310; FXYD; 1.
KW Hypothetical protein.
SQ SEQUENCE 92 AA; 10447 MW; 42244DD050C60A3B CRC64;

Query Match 28.5%; Score 131.5; DB 2; Length 92;
Best Local Similarity 38.2%; Pred. No. 4.8e-06;
Matches 29; Conservative 18; Mismatches 28; Indels 1; Gaps 1;

QY 1 MERVTLALL-LLAGLTALEANDPFANKDDPFYDWNQLQSLGICGGLLAIAAGIAVLGSK 60
DB 1 MASLSHILVLCVGLLAM-VNAEAPQEHDPFTYDQSLRIGGLIIAGILFILGILVLSRR 59

QY 61 CKYKSSQKOHSPVPEK 76
DB 60 CRCKFNQOQTGEPE 75

RESULT 14
PLM_HUMAN STANDARD; PRT; 92 AA.
ID_PLM_HUMAN
AC O00168;
DT 15-JUL-1998, integrated into UniProtKB/Swiss-Prot.
DT 30-AUG-2002, sequence version 2.
DT 07-FEB-2006, entry version 47.
DE Phospholemmann precursor (FXYD domain-containing ion transport
DE regulator 1).
GN Name=FXYD1; Synonyms=PLM;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RN NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Heart;
RC MEDLINE=97312702; PubMed=9169143; DOI=10.1006/geno.1997.4665;
RA Chen L.-S.K., Lo C.F., Numann R., Cuddy M.;
RA "Characterization of the human and rat phospholemmann (PLM) cDNAs and
RA localization of the human PLM gene to chromosome 19q13.1.";
RN Genomics 41:435-443(1997).
[2]
RN NUCLEOTIDE SEQUENCE [MRNA].
RC MEDLINE=20408885; PubMed=10950925; DOI=10.1006/geno.2000.6274;
RA Sweadner K.J., Rael E.;
RA "The FXYD gene family of small ion transport regulators or channels:
RA cDNA sequence, protein signature sequence, and expression.";
RN Genomics 68:41-56(2000).
[3]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Brain, Lung, and Testis;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
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DR PROSITE: PS01310; FXVD: 1.  
KW Chloride; Chloride channel; Ion transport; Ionic channel; Membrane;  
KW Signal; Transmembrane; Transport.  
FT SIGNAL 1 20 Potential.  
FT CHAIN 21 87  
FT TOPO DOM 21 38  
FT TRANSMEM 39 59  
FT TOPO DOM 60 87  
FT CONFLICT 36 37  
FT CONFLICT 58 58  
FT SEQUENCE 87 AA; 9263 MW; 6D674D668EB32493 CRC64;  
Query Match 46.5%; Score 214.5; DB 1; Length 87;  
Best Local Similarity 54.5%; Pred. No. 5.9e-15;  
Matches 48; Conservative 11; Mismatches 24; Indels 5; Gaps 4;  
QY 1 MERVTLALLL-LAGLTALANDPPFANKDDPPYDWNKQLSLGICGGLIATAGIAVLG 59  
Db 1 MOKVTLGLLVLAGFPVLDAND-LEDKNSPFYDWHSLQVGLICAGVLCAMGIIIVMSA 59  
QY 60 KCKYKSSQKQ-HSPVPEKAIPITPGSA 86  
Db 60 KCKCKFGQSGHH--PGTPTPLITPGSA 85  
RESULT 11  
Q61B59 HUMAN  
ID Q61B59 HUMAN PRELIMINARY; PRT; 87 AA.  
AC Q61B59  
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.  
DT 10-MAY-2005, sequence version 1.  
DT 07-FEB-2006, entry version 7.  
DE FXVD3 protein (FXVD domain containing ion transport regulator 3,  
isoform 1).  
GN Name=FXVD3;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Halleck A., Ebert L., Moundinya M., Schick M., Eisenstein S.,  
RA Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W.,  
RA Korn B., Zuo D., Hu Y., LaBaer J.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RA Kalline N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,  
RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,  
RA Phelan M., Farmer A.;  
RT "Cloning of human full-length CDSS in BD Creator(TM) System Donor  
vector";  
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=White Matter pool- 5 brain tissues- femoral artery;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Diatchenko L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences";  
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [5]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=White Matter pool- 5 brain tissues- femoral artery;  
RA Director MGC Project;  
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.  
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CC  
EMBL: CR456945; CAG33226.1; -; mRNA.  
DR EMBL; CR542197; CAG46994.1; -; mRNA.  
DR EMBL; BT006712; AAP35358.1; -; mRNA.  
DR EMBL; BC090044; AAH90044.1; -; mRNA.  
DR Ensembl; ENSG0000089356; Homo sapiens.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005216; F:ion channel activity; IEA.  
DR GO; GO:0006811; P:ion transport; IEA.  
DR InterPro; IPR00272; FXVD.  
DR Pfam; PF02038; ATP1G1\_PLM\_MAT8; 1.  
DR PROSITE; PS01310; FXVD; 1.  
SQ SEQUENCE 87 AA; 9263 MW; 6D674D668EB32493 CRC64;  
Query Match 46.5%; Score 214.5; DB 2; Length 87;  
Best Local Similarity 54.5%; Pred. No. 5.9e-15;  
Matches 48; Conservative 11; Mismatches 24; Indels 5; Gaps 4;  
QY 1 MERVTLALLL-LAGLTALANDPPFANKDDPPYDWNKQLSLGICGGLIATAGIAVLG 59  
Db 1 MOKVTLGLLVLAGFPVLDAND-LEDKNSPFYDWHSLQVGLICAGVLCAMGIIIVMSA 59  
QY 60 KCKYKSSQKQ-HSPVPEKAIPITPGSA 86  
Db 60 KCKCKFGQSGHH--PGTPTPLITPGSA 85  
RESULT 12  
Q80UV3 MOUSE  
ID Q80UV3\_MOUSE PRELIMINARY; PRT; 70 AA.  
AC Q80UV3;  
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.  
DT 01-JUN-2003, sequence version 1.  
DT 07-FEB-2006, entry version 13.  
DE Fxyd3 protein.  
GN Name=Fxyd3;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridea; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=FVB/N; TISSUE=Mammary tumor. Metallothionien-TGF alpha model.  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Diatchenko L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	
RESULT 9				
FXVD3 PIG				
ID	FXVD3	PIG	STANDARD;	PRT; 88 AA.
AC	O97797;			
DT	23-JAN-2002,	integrated into UniProtKB/Swiss-Prot.		
DT	01-MAY-1999,	sequence version 1.		
DT	07-FEB-2006,	entry version 32.		
DE	FXVD domain-containing ion transport regulator 3 precursor (Chloride			
DE	conductance inducer protein Mat-8) (Mammary tumor 8 kda protein).			
GN	Name=FXVD3; Synonyms=MAT8;			
OS	Sus scrofa (Pig).			
OC	Eukaryota; Metazoa;			
OC	Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;			
OC	Sus.			
OX	NCBI_TaxID=9823;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE [MRNA].			
RC	TISSUE=Gastric mucosa;			
RX	MEDLINE=99140476; PubMed=10206733;			
RA	Maeda M., Hamano K., Hirano Y., Suzuki M., Takahashi E., Terada T.,			
RA	Futai M., Sato R.;			
RT	"Structures of P-type transporting ATPases and chromosomal locations			
RT	of their genes."			
RL	Cell Struct. Funct. 23:315-323(1998).			
CC	-!- FUNCTION: Induces a hyperpolarization-activated chloride current			
CC	when expressed in Xenopus oocytes. May be a modulator capable of			
CC	activating endogenous oocyte channels.			
CC	-!- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane			
CC	protein (Potential).			
CC	-!- SIMILARITY: Belongs to the FXVD family.			
CC	Copyrighted by the UniProt Consortium, see <a href="http://www.uniprot.org/terms">http://www.uniprot.org/terms</a>			
CC	Distributed under the Creative Commons Attribution-NoDerivs License			
CC	-----			
DE	EMBL; AB015759; BAA35078.1; -; mRNA.			
DR	InterPro; IPR000272; FXVD.			
DR	Pfam; PF02038; ATP1G1_PLM_MAT8; 1.			
DR	PROSITE; PS01310; FXVD_1			
KW	Chloride; Chloride channel; Ion transport; Ionic channel; Membrane;			
KW	Signal; Transmembrane; Transport.			
FT	SIGNAL	1	17	Potential.
FT	CHAIN	18	88	FXVD domain-containing ion transport
FT				regulator 3.
FT				/FTid=PRO_0000010364.
FT	TOPO_DOM	18	38	Extracellular (Potential).
FT	TRANSMEM	39	59	Potential.
FT	TOPO_DOM	60	88	Cytoplasmic (Potential).
SQ	SEQUENCE	88 AA;	9314 MW;	6CC7810B90512E5A CRC64;
Query Match		50.0%;	Score 230.5;	DB 1; Length 88;
Best Local Similarity		57.8%;	Pred. No. 1.2e-16;	
Matches	52;	Conservative	10;	Mismatches 25; Indels 3; Gaps 3;
QY	1	MERVTLA-LLLAGLTALEANDPFANKDDPFYDWNQLQSLGICGGLLAIGIAAVLSG	59	
Db	1	MHEVALSVLLLAGLSALDNDP-EDKNSPFYDWHSLRVGLICAGTPCALGIILLSG	59	
QY	60	KCKYKSQKQHSVPVEKAIPLITPGSATTC	89	
Db	60	KCKCKFSQKP-SHRPGDAPPLITPGSAHNC	88	
RESULT 10				
FXVD3 HUMAN				
ID	FXVD3	HUMAN	STANDARD;	PRT; 87 AA.
AC	Q14802;			
DT	15-JUL-1998,	integrated into UniProtKB/Swiss-Prot.		
DT	01-NOV-1996,	sequence version 1.		
DT	07-FEB-2006,	entry version 48.		





DR GO: GO:0016021; C-integral to membrane; TAS.  
DR InterPro: IPR000272; FXD.  
DR Pfam: PF02038; ATP1G1\_PLM\_MAT8; 1.  
DR PROSITE: PS01310; FXD; 1.  
KW Chloride; Chloride channel; Ion transport; Ionic channel; Membrane;  
KW Signal; Transmembrane; Transport.  
FT SIGNAL 1 20 Potential.  
FT CHAIN 21 88 FXD domain-containing ion transport  
FT regulator 3.  
FT /FTid:PRO 0000010363.  
FT Extracellular (Potential).  
FT TOPO DOM 21 38  
FT TRANSMEM 39 59 Potential.  
FT TOPO DOM 60 88 Cytoplasmic (Potential).  
SQ SEQUENCE 88 AA; 9526 MW; 9CD61684E85E35D CRC64;  
Query Match 52.4%; Score 241.5; DB 1; Length 88;  
Best Local Similarity 57.8%; Pred. No. 7.6e-18;  
Matches 52; Conservative 11; Mismatches 24; Indels 3; Gaps 3;  
QY 1 MERVTLALL-LIAGLTALANDPFAKDDPFYYDWNKQLSCGLLAIGIAVLSG 59  
| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| : |||  
Db 1 MQEVLSSLVLLAGLTDLANDP-ENKNDPFYYDWSLRVGGILCALGIIIVMSG 59  
QY 60 KCKYKSSQKHSPVPEKAIPLIIPGSATTC 89  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 60 KCKKPRQRP-SHRPGGPPLIIPGSAHNC 88  
RESULT 7  
ID Q3TLM3\_MOUSE PRELIMINARY; PRT; 88 AA.  
AC Q3TLM3;  
DT 11-OCT-2005, integrated into UniProtKB/TREMBL.  
DT 11-OCT-2005, sequence version 1.  
DT 07-FEB-2006, entry version 5.  
DE Mammary gland RCB-0527 Jyg-MC(B) cDNA, RIKEN full-length enriched  
DE library, clone:G930017D12 product:FXD domain-containing ion transport  
DE regulator 3, full insert sequence (Mammary gland RCB-0527 Jyg-MC(B)  
DE cDNA, RIKEN full-length enriched library, clone:G930019M21  
DE product:FXD domain-containing ion transport regulator 3, full insert  
DE sequence).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muroidae; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX TISSUE=Mammary gland;  
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning.";  
RL Methods Enzymol. 303:19-44(1999).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX TISSUE=Mammary gland;  
RX PubMed=16141072; DOI=10.1126/science.1112014;  
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,  
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,  
RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,  
RA Davis M.J., Wilming L.G., Aldins V., Allen J.E.,  
RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,  
RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,  
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,  
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,  
RA di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,  
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,  
RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,  
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,  
RA Hilt M., Humnicki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,  
RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,  
RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,  
RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,

Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,  
RA Matsuura H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,  
RA Motagui-Tabar S., Mulder N., Nakano N., Nishikawa S., Nori F., Ohara O.,  
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,  
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavoni G., Pease G.,  
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,  
RA Rost B., Ruan Y., Salzberg S.L., Sanderlin A., Schneider C.,  
RA Schonbach C., Sekiguchi K., Semple C.A., Sessa L., Sheng Y.,  
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,  
RA Sperling S., Stupka E., Sugitara K., Sultana R., Takenaka Y., Taki K.,  
RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,  
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,  
RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,  
RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,  
RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,  
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,  
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,  
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,  
RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,  
RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,  
RA Hayashizaki Y.;  
RT "The transcriptional landscape of the mammalian genome.";  
RL Science 309:1559-1563(2005).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Mammary gland;  
RX PubMed=16141073; DOI=10.1126/science.1112009;  
RG RIKEN Genome Exploration Research Group, and Genome Science Group  
RG (Genome Network Core Team) and the FANTOM Consortium;  
RT "Antisense Transcription in the Mammalian Transcriptome.";  
RL Science 309:1564-1566(2005).  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Mammary gland;  
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kiyosawa H.,  
RA Nikaido I., Oatso N., Saito R., Suzuki H., Yamanaka I., Miyosawa H.,  
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frizer K.S.,  
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
RA Sanderlin A., Schneider C., Semple C.A., Setou M., Shimada K.,  
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,  
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
RA Birney E., Hayashizaki Y.;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
RN [5]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Mammary gland;  
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishikawa K., Kiyosawa H., Kondo S., Yamanaka I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuura H.A., Ashburner M., Batalov S., Casavant T.,

DE inducing factor) (CHIP) (Corticosteroid-induced protein).

GN Name=Fxyd4;

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Muridae; Murinae; Rattus.

ON NCBI\_TaxID=10116;

RN [1]

RP NUCLEOTIDE SEQUENCE [mRNA].

RC STRAIN=Wistar; TISSUE=Colon.

RX MEDLINE=95320221; PubMed=7597086;

RA Attali B., Lattier H., Rachani N., Garty H.;

RT "A corticosteroid-induced gene expressing an 'Isk-like' K<sup>+</sup> channel

RT activity in Xenopus oocytes";

RL Proc. Natl. Acad. Sci. U.S.A. 92:6092-6096(1995).

RN [2]

RP TISSUE SPECIFICITY.

RX MEDLINE=97000648; PubMed=8843704;

RA Capurro C., Couty N., Bonvalet J.-P., Escoubet B., Garty H.,

RA Farman N.;

RT "Cellular localization and regulation of CHIP in kidney and colon";

RL Am. J. Physiol. 271:C753-C762(1996).

CC -!- FUNCTION: Induces a potassium channel when expressed in Xenopus

CC oocytes.

CC -!- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane

CC protein (Potential).

CC -!- TISSUE SPECIFICITY: Selectively present in the distal parts of the

CC nephron (medullary and papillary collecting ducts and end portions

CC of cortical collecting tubule) and in the epithelial cells of the

CC distal colon. No expression is found in renal proximal tubule,

CC loop of henle and distal tubule, proximal colon, small intestine,

CC lung, choroid plexus, salivary glands, or brain.

CC -!- INDUCTION: By corticosteroids.

CC -!- SIMILARITY: Belongs to the FXYD family.

CC

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CC

DR EMBL: L41254; AA0474691.1; -; mRNA.

DR PIR: I59391; I59391.

DR Ensembl: ENSRNOG0000014578; Rattus norvegicus.

DR RGD: 70998; Fxyd4.

DR GO: GO:0005267; F:potassium channel activity; IDA.

DR InterPro: IPR000272; FXYD.

DR Pfam: PF02038; ATP1G1\_PLM\_MAT8; 1.

DR PROSITE: PS01310; FXYD; 1.

DR Ion transport; Ionic channel; Membrane; Signal; Transmembrane;

KW Transport.

FT SIGNAL 1 20 Potential.

FT CHAIN 21 87 FXYD domain-containing ion transport

FT regulator 4.

FT /FTID=PRO\_000010368.

FT TOPO\_DOM 21 38 Extracellular (Potential).

FT TRANSMEM 39 59 Potential.

FT TOPO\_DOM 60 87 Cytoplasmic (Potential).

SQ SEQUENCE 87 AA; 9084 MW; 5D0D81F6C6B1BCCA CRC64;

Query Match 55.6%; Score 256.5; DB 1; Length 87;

Best Local Similarity 61.5%; Pred. No. 1.9e-19;

Matches 56; Conservative 11; Mismatches 17; Indels 7; Gaps 4;

QY 1 MERVTLA-LLLAGLTALEANDPPFANKDDPFYDWNKQLSLGGLAINGIAAVLSG 59

Db 1 MEGITCAFLVLAGLVLEANGP-VDRKSPFYDWSLQGMIFGGLCTAGIAVALSG 59

QY 60 KCKYKSSQKQHP--VPEKAIPLIPTGSATT 88

Db 60 KCK---CRRNHTPSSLPEKVTLLIPTGSAST 87

RESULT 6

FXYD3\_MOUSE

ID FXYD3\_MOUSE STANDARD; PRT; 88 AA.

AC Q61835;

DT 15-JUL-1998, integrated into UniProtKB/Swiss-Prot.

DT 01-NOV-1996, sequence version 1.

DT 07-FEB-2006, entry version 49.

DE FXYD domain-containing ion transport regulator 3 precursor (Chloride

DE conductance inducer protein Mat-8) (Mammary tumor 8 kDa protein)

DE (Phospholemman-like).

DE Name=Fxyd3; Synonyms=Mat8, Plml;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muroidae; Muridae; Murinae; Mus.

ON NCBI\_TaxID=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE [mRNA].

RC STRAIN=FVB/N; TISSUE=Mammary gland;

RX MEDLINE=95060797; PubMed=7970700;

RA Morrison B.W., Leder P.;

RT "neu and ras initiate murine mammary tumors that share genetic markers

RT generally absent in c-myc and int-2-initiated tumors.";

RL Oncogene 9:3417-3426(1994).

RN [2]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

RC TISSUE=Mammary tumor;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [3]

RP EXPRESSION.

RX MEDLINE=95138184; PubMed=7836447; DOI=10.1074/jbc.270.15.8571;

RA Morrison B.W., Moorman J.R., Kowdley G.C., Kobayashi Y.M., Jones L.R.,

RA Leder P.;

RT "Mat-8, a novel phospholemman-like protein expressed in human breast

RT tumors, induces a chloride conductance in Xenopus oocytes.";

RL J. Biol. Chem. 270:2176-2182(1995).

CC -!- FUNCTION: Induces a hyperpolarization-activated chloride current

CC when expressed in Xenopus oocytes. May be a modulator capable of

CC activating endogenous oocyte channels.

CC -!- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane

CC protein (Potential).

CC -!- TISSUE SPECIFICITY: Expressed in a subset of murine breast tumors.

CC -!- MISCELLANEOUS: Marker of a cell type preferentially transformed by

CC neu or ras oncoprotein.

CC -!- SIMILARITY: Belongs to the FXYD family.

CC

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CC

DR EMBL: X93038; CAA63606.1; -; mRNA.

DR EMBL: BC020239; AA020239.1; -; mRNA.

DR EMBL: BC056223; AA056223.1; -; mRNA.

DR PIR: S61552; S61552.

DR Ensembl: ENSMUSG00000057092; Mus musculus.

DR MGI: MGI:107497; Fxyd3.

DR GO: GO:0005615; C:extracellular space; TAS.

QY 1 MERVTLALLAGLTALEANDPANKDPFYDWNKQLSLGICGGLLAIAIAVLGSK 60  
 DB 1 MERVTLALLAGLTALEANDPANKDPFYDWNKQLSLGICGGLLAIAIAVLGSK 60  
 QY 61 CKYKSSQKQHSVPVPEKAIPITPGSATTC 89  
 DB 61 CKKSSQKQHSVPVPEKAIPITPGSATTC 89  
 RESULT 4  
 ID FXYD4 MOUSE  
 AC FXYD4 MOUSE STANDARD; PRT; 88 AA.  
 DT 23-JAN-2002, integrated into UniProtKB/Swiss-Prot.  
 DT 01-JUN-2001, sequence version 1.  
 DT 07-FEB-2006, entry version 28.  
 DE FXYD domain-containing ion transport regulator 4 precursor (Channel-  
 DE inducing factor) (CHIF).  
 GN Name=Fxyd4,  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridea; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=129/SvJ;  
 RA Garty H.;  
 RL "Genomic sequence of mouse CHIF (FXYD4).";  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 [2]  
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 RC STRAIN=C57BL/6J; TISSUE=Kidney;  
 RX PubMed=1641072; DOI=10.1126/science.11112014;  
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,  
 RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,  
 RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,  
 RA Davis M.J., Wilming L.G., Altinis V., Allen J.E.,  
 RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,  
 RA Bansal M., Baxter L., Belsel K.W., Bersano T., Bono H., Chalk A.M.,  
 RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,  
 RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,  
 RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,  
 RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,  
 RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,  
 RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,  
 RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelson J., Kitamura H.,  
 RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,  
 RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,  
 RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,  
 RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,  
 RA Mottagui-Tabar S., Mulder N., Nakano N., Nakaguchi H., Ng P.,  
 RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,  
 RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavoni G., Pesole G.,  
 RA Petrovsky N., Piazza S., Reed J.F., Reid J.F., Ring B.Z., Ringwald M.,  
 RA Rost B., Ruan Y., Salzberg S.L., Sanderlin A., Schneider C.,  
 RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L.,  
 RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,  
 RA Sperling S., Stupka E., Sugura K., Sultana R., Takenaka Y., Taki K.,  
 RA Tammoja K., Tan S.B., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,  
 RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,  
 RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,  
 RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,  
 RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,  
 RA Fukuda S., Kanamori-Katayama M., Suzuki M., Roki J., Arakawa T.,  
 RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,  
 RA Kawaohima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,  
 RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,  
 RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,  
 RA Hayaehizaki Y.;  
 RT "the transcriptional landscape of the mammalian genome.";  
 RL Science 309:1559-1563(2005).

[3]  
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 RC TISSUE=Kidney;  
 RX MEDLINE=238257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Frange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -!- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane  
 CC protein (Potential).  
 CC -!- SIMILARITY: Belongs to the FXYD family.  
 CC  
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 CC  
 DR EMBL: AF362729; AAKS1508.1; -; Genomic DNA.  
 DR EMBL: AK018728; BAB31372.1; -; mRNA.  
 DR EMBL: BC086918; AAB86918.1; -; mRNA.  
 DR Ensembl: ENSMUSG0000004988; Mus musculus.  
 DR MGI: MGI:1889005; Fxyd4.  
 DR GO: GO:0005615; C:extracellular space; TAS.  
 DR GO: GO:0016021; C:integral to membrane; TAS.  
 DR InterPro: IPR000272; FXYD.  
 DR Pfam: PF02038; ATP1G\_PLM\_MAT8; 1.  
 DR PROSITE: PS01310; FXYD; 1.  
 KW Ion transport; Ionic channel; Membrane; Signal; Transmembrane;  
 KW Transport.  
 FT SIGNAL 1 20 Potential  
 FT CHAIN 21 88 FXYD domain-containing ion transport  
 FT regulator 4.  
 FT /FTID=PRO\_0000010367.  
 FT TOPO\_DOM 21 38 Extracellular (Potential).  
 FT TRANSMEM 39 59 Potential.  
 FT TOPO\_DOM 60 88 Cytoplasmic (Potential).  
 FT SEQUENCE 88 AA; 9269 MW; 7EB0140941CFE926 CRC64;  
 SQ  
 Query Match 60.0%; Score 276.5; DB 1; Length 88;  
 Best Local Similarity 66.7%; Pred. No. 1.4e-21;  
 Matches 60; Conservative 8; Mismatches 19; Indels 3; Gaps 3;  
 QY 1 MERVTLA-LLLAGLTALEANDPANKDPFYDWNKQLSLGICGGLLAIAIAVLGSK 59  
 DB 1 MBEITCAFLLLAGLPALEASDP-VDKDSPFYDWNKQLSLGICGGLLAIAIAVLGSK 59  
 QY 60 KCKYKSSQKQHSVPVPEKAIPITPGSATTC 89  
 DB 60 KCKCRTHKP-SLPGKATPLIPGSANTC 88  
 RESULT 5  
 ID FXYD4 RAT  
 AC Q63113;  
 DT 15-JUL-1998, integrated into UniProtKB/Swiss-Prot.  
 DT 01-NOV-1996, sequence version 1.  
 DT 07-FEB-2006, entry version 39.  
 DE FXYD domain-containing ion transport regulator 4 precursor (Channel-

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Q724M5 HUMAN
ID Q724M5 HUMAN PRELIMINARY; PRT; 89 AA.
AC Q724M5;
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2003, sequence version 1.
DE FXD domain containing ion transport regulator 4.
DE Name=FXD4; ORFNames=RP11-92P6.2-004;
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX Strausberg R.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX Corby N.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; BC054876; AAH54876.1; -; mRNA.
DR EMBL; AL512654; CA117065.1; -; Genomic DNA.
DR Ensembl; ENSG00000150201; Homo sapiens.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005216; F:ion channel activity; IEA.
DR GO; GO:0008811; P:ion transport; IEA.
DR InterPro; IPR000272; FXD.
DR Pfam; PF02038; ATP1G1_PLM_MAT8; 1.
DR PROSITE; PS01310; FXD; 1.
SQ SEQUENCE 89 AA; 9373 MW; C5935929A22449B0 CRC64;

Query Match 98.0%; Score 452; DB 2; Length 89;
Best Local Similarity 98.9%; Pred.No. 2.e-40;
Matches 88; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MERVTLALLLGLAGLTALEANDPFANKDPFYDWKNQLSLGICGLLAIAIAVLGSK 60
DB 1 MERVTLALLLGLAGLTALEANDPFANKDPFYDWKNQLSLGICGLLAIAIAVLGSK 60

QY 61 CKYKSSQKQHSVPVPEKAIPLIIPGSAATC 89
DB 61 CKYKSSQKQHSVPVPEKAIPLIIPGSAATC 89

Query Match 97.6%; Score 450; DB 1; Length 89;
Best Local Similarity 97.8%; Pred.No. 3.6e-40;
Matches 87; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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1419 56.5 12.3 567 2 04KI08\_PSEF5  
1420 56.5 12.3 570 2 04WD85\_ASPFU  
1421 56.5 12.3 577 2 08SQSO\_9INSE  
1422 56.5 12.3 580 2 03HIY1\_TRIER  
1423 56.5 12.3 589 2 02WSX0\_CLOBE  
1424 56.5 12.3 595 1 S13A1\_HUMAN  
1425 56.5 12.3 608 2 09BAR2\_9MAGN  
1426 56.5 12.3 611 2 03AEG0\_CARBZ  
1427 56.5 12.3 614 2 031615\_BACSU  
1428 56.5 12.3 624 2 069290\_MOUSE  
1429 56.5 12.3 648 2 05FUH5\_GLUOX  
1430 56.5 12.3 666 2 04COA1\_CROST  
1431 56.5 12.3 670 2 032212\_BACSU  
1432 56.5 12.3 681 2 09BAQ3\_9MAGN  
1433 56.5 12.3 683 2 05CV27\_CRYPV  
1434 56.5 12.3 688 2 09BAS3\_9MAGN  
1435 56.5 12.3 686 1 VGLH\_PRVK  
1436 56.5 12.3 686 1 VGLH\_PRVN3  
1437 56.5 12.3 686 1 VGLH\_PRVRI  
1438 56.5 12.3 686 2 05PPA2\_9ALPH  
1439 56.5 12.3 688 2 09BAS8\_9MAGN  
1440 56.5 12.3 689 2 07Q3N1\_ANOGA  
1441 56.5 12.3 690 2 09BAS4\_9MAGN  
1442 56.5 12.3 690 2 09BAS2\_9MAGN  
1443 56.5 12.3 691 2 09BAQ8\_BUXSE  
1444 56.5 12.3 692 2 09BAQ9\_9MAGN  
1445 56.5 12.3 692 2 09BAS5\_9MAGN  
1446 56.5 12.3 692 2 09BAS5\_9MAGN  
1447 56.5 12.3 692 2 09BAS7\_9MAGN  
1448 56.5 12.3 695 2 09BAS7\_9MAGN  
1449 56.5 12.3 699 2 096SW4\_HUMAN  
1450 56.5 12.3 704 2 09SC14\_BUXSE  
1451 56.5 12.3 707 2 09BAS6\_9MAGN  
1452 56.5 12.3 710 2 06CCN0\_YARLI  
1453 56.5 12.3 721 2 03KK27\_PSRPF  
1454 56.5 12.3 726 2 08HTM7\_PODPE  
1455 56.5 12.3 726 2 08HTM9\_9MAGN  
1456 56.5 12.3 726 2 08HTM9\_9MAGN  
1457 56.5 12.3 729 2 05PXK6\_RAT  
1458 56.5 12.3 730 2 05PXK5\_RAT  
1459 56.5 12.3 757 1 KCNC3\_HUMAN  
1460 56.5 12.3 758 2 0811T2\_RAT  
1461 56.5 12.3 759 2 08HXV1\_RABIT  
1462 56.5 12.3 769 2 0811T3\_RAT  
1463 56.5 12.3 783 2 05NXT1\_AZOSE  
1464 56.5 12.3 809 2 02LQ19\_9DELT  
1465 56.5 12.3 852 1 YKM1\_YEAST  
1466 56.5 12.3 856 2 03KJ08\_PSRPF  
1467 56.5 12.3 856 2 06G429\_BARHE  
1468 56.5 12.3 889 1 KCNC3\_RAT  
1469 56.5 12.3 894 2 05CGN7\_CRYHO  
1470 56.5 12.3 918 2 04DX98\_TRYCR  
1471 56.5 12.3 933 2 083GL1\_TROWT  
1472 56.5 12.3 939 2 083HL6\_TROW8  
1473 56.5 12.3 1000 2 05U635\_HUMAN  
1474 56.5 12.3 1009 2 05Q208\_IDILO  
1475 56.5 12.3 1023 2 043X28\_SOLUS  
1476 56.5 12.3 1030 1 SEMGA\_HUMAN  
1477 56.5 12.3 1044 2 04CTU4\_TRYCR  
1478 56.5 12.3 1058 2 05P5T6\_AZOSE  
1479 56.5 12.3 1127 2 04YF05\_PLABE  
1480 56.5 12.3 1241 2 060RT2\_CAEER  
1481 56.5 12.3 1250 2 04PIV2\_USTWA  
1482 56.5 12.3 1643 2 05ZCR4\_ORYSA  
1483 56.5 12.3 1739 2 04SXM5\_TETNG  
1484 56.5 12.3 1778 2 041AN8\_GIBZE  
1485 56.5 12.3 1780 2 048P50\_PSEI4  
1486 56.5 12.3 1838 2 06BCJ9\_TETTH  
1487 56.5 12.3 1844 2 05BDW2\_EMENI  
1488 56.5 12.3 2113 2 04RMA1\_TETNG  
1489 56.5 12.3 2217 1 DPOE\_CANGA  
1490 56.5 12.3 2876 2 04Q873\_LEIMA  
1491 56.5 12.3 4464 2 07RL36\_PLAYO

1492 56 12.1 75 2 08E590\_STR3  
1493 56 12.1 79 1 IVBKI\_DENPO  
1494 56 12.1 100 2 06N984\_RHOPA  
1495 56 12.1 102 2 04AV09\_9BURK  
1496 56 12.1 103 1 NIRC\_PARDE  
1497 56 12.1 103 2 03PA73\_PARDE  
1498 56 12.1 103 2 08K2N1\_MOUSE  
1499 56 12.1 117 2 03IPT2\_NATPD  
1500 56 12.1 118 2 02JLN1\_9CYAN

Q8E590 streptococ  
P00981 dendroaspis  
Q6N984 rhodopseudo  
Q4AV09 pollaromonas  
Q51702 paracoccus  
Q3PA73 paracoccus  
Q8K2N1 mus musculus  
Q3IPT2 natronomona  
Q2JLN1 cyanobacter

ALIGNMENTS

RESULT 1  
Q6UWZ1 HUMAN PRELIMINARY; PRT; 89 AA.  
ID Q6UWZ1 HUMAN PRELIMINARY; PRT; 89 AA.  
AC Q6UWZ1;  
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.  
DT 05-JUL-2004, sequence version 1.  
DT 07-FEB-2006, entry version 11.  
DE ERVTS26.  
GN Homo sapiens (Human).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22687296; PubMed=12975309; DOI=10.1101/gr.1293003;  
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,  
Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,  
Eaton D., Foster H.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,  
Huang A., Kim H.S., Klinowski L., Jin Y., Johnson S., Lee J.,  
Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,  
Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,  
Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,  
Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,  
Wood W.I., Godowski P.J., Gray A.M.;  
RT "The secreted protein discovery initiative (SPDI), a large-scale  
effort to identify novel human secreted and transmembrane proteins: a  
bioinformatics assessment."  
RL Genome Res. 13:2265-2270(2003).  
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CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC  
CC EMBL; AY358584; AAQ88947.1; -; mRNA.  
DR Ensembl; ENSG00000150201; Homo sapiens.  
DR HGNC; HGNC:4028; FXFD4.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005216; F:ion channel activity; IEA.  
DR GO; GO:0006811; P:ion transport; IEA.  
DR InterPro; IPR000272; FXFD.  
DR Pfam; PF02038; ATP1G1\_PLM\_MAT8; 1.  
DR PROSITE; PS01310; FXFD; 1.  
SQ SEQUENCE 89 AA; 9433 MW; C5934288182449B0 CRC64;

Query Match 100.0%; Score 461; DB 2; Length 89;  
Best Local Similarity 100.0%; Pred. No. 2.4e-41;  
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERVTLALLLLAGLTALEANDPFANKDDPFYDWNKQLSGLICGGLAIAVLSGK 60  
Db 1 MERVTLALLLLAGLTALEANDPFANKDDPFYDWNKQLSGLICGGLAIAVLSGK 60  
QY 61 CKYKSKQKQHSVPPEKAIIITPGSATTC 89  
Db 61 CKYKSKQKQHSVPPEKAIIITPGSATTC 89

RESULT 2



1273	57	12.4	1574	2	Q7Y5J5_9CAUD	Q7v5j5	xanthomonas
1274	57	12.4	1639	2	Q54J43_DICDI	Q54j43	dictyosteli
1275	57	12.4	1875	2	Q5X8U3_LEGPA	Q5x8u3	legionella
1276	57	12.4	2660	2	Q7QL19_ANGA	Q7ql19	anopheles g
1277	57	12.4	3196	2	Q6ALQ5_DESPS	Q6alq5	desulfotale
1278	57	12.4	3338	2	Q82PH6_STRAW	Q82ph6	streptomyce
1279	56.5	12.3	104	2	Q6J2H4_PSEYM	Q6j2h4	pseudomonas
1280	56.5	12.3	107	2	Q67MA1_SYNTH	Q67ma1	symbiobacte
1281	56.5	12.3	110	2	Q6J932_9LILI	Q6j932	xerophyta h
1282	56.5	12.3	114	1	HXD3_RAT	P18867	rattus norv
1283	56.5	12.3	118	2	Q3BH53_PLAFA	Q3bh53	plasmodium
1284	56.5	12.3	120	2	Q6JIA6_HUMAN	Q6jia6	homo sapien
1285	56.5	12.3	120	2	Q4MPP5_BACCE	Q4mpp5	bacillus ce
1286	56.5	12.3	120	2	Q63EV5_BACCZ	Q63ev5	bacillus ce
1287	56.5	12.3	120	2	Q6HMB7_BACHK	Q6hmb7	bacillus th
1288	56.5	12.3	120	2	Q81U42_BACAN	Q81u42	bacillus an
1289	56.5	12.3	131	2	Q3DXU3_CHLAU	Q3dxu3	chloroflexu
1290	56.5	12.3	143	2	Q8PLW5_XANAC	Q8plw5	xanthomonas
1291	56.5	12.3	145	2	Q75LT0_HUMAN	Q75lt0	homo sapien
1292	56.5	12.3	145	2	Q8E9G4_LYNST	Q8e9g4	lynnaea sta
1293	56.5	12.3	148	2	Q99LS0_MOUSE	Q99ls0	mus musculus
1294	56.5	12.3	148	2	Q9D2U7_MOUSE	Q9d2u7	m adult mal
1295	56.5	12.3	167	2	Q34YP4_9GAMM	Q34yp4	alkalilimi
1296	56.5	12.3	170	2	Q9W2N2_DROME	Q9w2n2	drosophila
1297	56.5	12.3	178	2	Q2VM44_9LILI	Q2vm44	xerophyta h
1298	56.5	12.3	186	2	Q6NL91_RHOBA	Q6nl91	rhodopseudo
1299	56.5	12.3	187	2	Q3YTK2_SHIFF	Q3ytk2	shigella eo
1300	56.5	12.3	187	2	Q52296_SHIFF	Q52296	shigella fl
1301	56.5	12.3	187	2	Q7BEL2_SHIFL	Q7bel2	shigella fl
1302	56.5	12.3	188	2	Q5FRN2_GLUOX	Q5frn2	gluconobact
1303	56.5	12.3	190	2	Q9JKW1_RAT	Q9jkw1	rattus norv
1304	56.5	12.3	191	2	Q5J7F1_SALCH	Q5j7f1	salmonella
1305	56.5	12.3	191	2	Q5PLD9_SALPA	Q5pld9	salmonella
1306	56.5	12.3	191	2	Q7CPPO_SALTY	Q7cpo0	salmonella
1307	56.5	12.3	191	2	Q8XGY6_SALTI	Q8xgy6	salmonella
1308	56.5	12.3	194	1	TIM22_MOUSE	Q9c85	mus musculus
1309	56.5	12.3	194	2	Q5SSL1_MOUSE	Q5sll1	mus musculus
1310	56.5	12.3	194	2	Q9JKW2_MOUSE	Q9jkw2	mus musculus
1311	56.5	12.3	195	2	Q8IN78_DROSOPHILA	Q8in78	drosophila
1312	56.5	12.3	197	2	Q8U0L2_PYRFU	Q8u0l2	pyrococcus
1313	56.5	12.3	197	2	Q73KTE_TREDE	Q73kte6	treponema d
1314	56.5	12.3	198	2	Q3R4M1_XYLFA	Q3r4m1	xyella fas
1315	56.5	12.3	198	2	Q3RFY3_XYLFA	Q3rfy3	xyella fas
1316	56.5	12.3	211	2	Q6EST5_FUGRU	Q6est5	fugu rubrip
1317	56.5	12.3	213	2	Q8NS64_CORGL	Q8ns64	corynebacte
1318	56.5	12.3	214	2	Q4V6C7_DROME	Q4v6c7	drosophila
1319	56.5	12.3	215	2	Q37HM5_RHOBA	Q37hm5	rhodopseudo
1320	56.5	12.3	228	2	Q84WK4_ARATH	Q84wk4	arabidopsis
1321	56.5	12.3	228	2	Q4Q087_CHLLI	Q4q087	chlorobium
1322	56.5	12.3	231	2	Q7ULW2_RHOBA	Q7ulw2	rhodopirell
1323	56.5	12.3	233	1	LPFX_MYCBO	P65307	mycobacteri
1324	56.5	12.3	233	1	LPFX_MYCTU	P65306	mycobacteri
1325	56.5	12.3	234	2	Q92LX9_RHIME	Q92lx9	rhizobium m
1326	56.5	12.3	240	2	Q3E033_CHLAU	Q3e033	chloroflexu
1327	56.5	12.3	244	2	Q8K2G6_MOUSE	Q8k2g6	mus musculus
1328	56.5	12.3	258	2	Q9HP14_HALSA	Q9hp14	halobacteri
1329	56.5	12.3	269	2	Q4D929_TRYCR	Q4d929	trypanosoma
1330	56.5	12.3	269	2	Q4E1D8_TRYCR	Q4e1d8	trypanosoma
1331	56.5	12.3	274	2	Q4SET1_TETNG	Q4set1	tetradon n
1332	56.5	12.3	276	2	Q937L7_9CYAN	Q937l7	uncultured
1333	56.5	12.3	276	2	Q937L8_9CYAN	Q937l8	uncultured
1334	56.5	12.3	277	2	Q39UV6_GEONG	Q39uv6	geobacter m
1335	56.5	12.3	288	2	Q37UN3_SPHAR	Q37un3	novosphingo
1336	56.5	12.3	288	2	Q38WC4_LACSS	Q38wc4	lactobacill
1337	56.5	12.3	288	2	Q826Y5_STRAW	Q826y5	streptomyce
1338	56.5	12.3	292	2	Q3WVQ4_9RHIZ	Q3wvq4	mesorhizob
1339	56.5	12.3	298	2	Q3F9W2_9BURK	Q3f9w2	burkholderi
1340	56.5	12.3	299	2	Q4SGT7_TETNG	Q4sgt7	tetradon n
1341	56.5	12.3	304	2	Q4H8A0_9DEIO	Q4h8a0	deinococcus
1342	56.5	12.3	304	2	Q2JDT3_9ACTO	Q2jdt3	frankia sp.
1343	56.5	12.3	305	2	Q5ZIU9_CHICK	Q5ziu9	gallus gall
1344	56.5	12.3	308	2	Q3AYC0_SYNS9	Q3ayc0	synecococc
1345	56.5	12.3	316	2	Q47SW6_THEFY	Q47sw6	thermobifid

Q2irs6	rhodopseudo
Q3lclj1	acidianus a
Q8g6m8	balidobacta e
Q46pc3	trypanosoma
Q90k55	trypanosoma
Q90k55	trypanosoma
Q46be6	solibacter
Q46sj4	ralstonia e
Q7uxc7	rhodopirell
Q60dt9	oryza sativ
Q4ukp7	rickettsia
Q2vqy9	anas platyr
Q5yva8	ustilago ma
Q5qnb2	oryza sativ
Q5q7hi	antheraea p
Q2rl15	moorella th
Q88110	pseudomonas
Q6mlc9	bdellovibri
Q81jg4	bacillus an
Q7qea4	anopheles g
Q8lrbe6	oryza sativ
Q7w0p4	borderella
Q7w3g0	borderella
Q7wet0	borderella
Q4j3y8	azotobacter
Q8eis5	shewanella
Q6lm16	photobacter
Q7p149	chromobacte
Q4bjh1	burkholderi
Q4ss40	tetradon n
Q2x2d9	shewanella
Q2zq35	shewanella
Q3q0h7	shewanella
Q44175	chromohalob
Q44175	chromohalob
P11838	cryphonectr
Q35wk9	shewanella
Q5bbs0	anaplasma m
Q4d416	trypanosoma
Q59h29	homo sapien
Q41r90	ferroplasma
Q5qx17	idiolmarina
Q2rxb3	rhodospiril
Q3imj0	synecococc
Q5mzd9	synecococc
Q2rua2	rhodospiril
Q3jy99	burkholderi
Q62g62	burkholderi
Q63pw6	burkholderi
Q49635	arabidopsis
Q2j1n41	cyanobacter
Q4zck1	bacterioph
Q55wa9	cryptococcu
Q86e12	drosophila
Q86e12	drosophila
Q97ka2	clostridium
Q9f10	myxococcus
Q8vdm1	mus musculu
Q7rw85	mus musculu
Q7ryh0	neurospora
Q567m8	brachydanio
Q38ac0	trypanosoma
Q38ab9	trypanosoma
Q06222	trypanosoma
Q38ab8	trypanosoma
Q3ufir6	mus musculu
Q4jxl7	corynebacte



1127	57	12.4	184	2	Q2NAP3_9SPHN	Q2nap3 erythroblast
1128	57	12.4	185	1	ADML_RAT	P43145 ratus norv
1129	57	12.4	190	1	PYRE_THETN	P58558 thermoanaer
1130	57	12.4	192	2	Q3N6V0_9PROT	Q3n6v0 nitrosomona
1131	57	12.4	203	2	Q3VRW3_PROAE	Q3vrw3 prosthococh
1132	57	12.4	215	2	Q5COA4_SCHJA	Q5coa4 schistosoma
1133	57	12.4	228	2	Q83TM7_LISMO	Q83tm7 listeria mo
1134	57	12.4	230	2	Q8EG49_SHEON	Q8eg49 shewanella
1135	57	12.4	232	2	Q3TYU9_MOUSE	Q3tyu9 mus musculus
1136	57	12.4	233	2	Q2YBT7_NITMU	Q2ybt7 nitrosospir
1137	57	12.4	241	2	Q658A8_ORYSA	Q658a8 oryza sativ
1138	57	12.4	249	2	Q3B7R5_BRARE	Q3b7r5 brachydanio
1139	57	12.4	254	2	Q61095_TRYCR	Q61095 trypanosoma
1140	57	12.4	254	2	Q3FST5_9BURK	Q3fst5 rhodofexax
1141	57	12.4	258	1	UDP_TREPA	Q83990 treponema p
1142	57	12.4	264	2	Q46QR2_RALEJ	Q46qr2 ralistonia e
1143	57	12.4	268	2	Q70FY9_9CVAN	Q70fy9 uncultured
1144	57	12.4	269	2	Q8YQW0_ANABE	Q8yqw0 anabaena sp
1145	57	12.4	276	2	Q68ES3_XENLA	Q68es3 xenopus lae
1146	57	12.4	281	2	Q3OWE1_DESDG	Q3owe1 desulfovibr
1147	57	12.4	283	2	Q4V7U2_XENLA	Q4v7u2 xenopus lae
1148	57	12.4	287	2	Q41VJ1_DESHA	Q41vj1 desulfitoba
1149	57	12.4	289	2	Q2XIL5_PSEPU	Q2xil5 pseudomonas
1150	57	12.4	291	2	Q5WX66_LEGPL	Q5wx66 legionella
1151	57	12.4	292	2	Q6UY47_HUMAN	Q6uy47 homo sapien
1152	57	12.4	292	2	Q3P8A6_PARDE	Q3p8a6 paracoccoc
1153	57	12.4	301	2	Q8BYJ2_MOUSE	Q8byj2 m adult mal
1154	57	12.4	302	2	Q2ZQT2_SHEPU	Q2zqt2 shewanella
1155	57	12.4	302	2	Q2ZS9J_SHEPU	Q2zsj9 shewanella
1156	57	12.4	302	2	Q768S4_MOUSE	Q768s4 mus musculus
1157	57	12.4	305	2	Q2X7G0_9GAMM	Q2x7g0 shewanella
1158	57	12.4	313	2	Q3OWA0_DESDG	Q3owa0 desulfovibr
1159	57	12.4	315	2	Q9UNE2_HUMAN	Q9une2 homo sapien
1160	57	12.4	325	2	Q9QN99_9VIRU	Q9qn99 rice grassy
1161	57	12.4	332	2	Q52M67_PAVLU	Q52m67 pavlova lut
1162	57	12.4	334	2	Q52W83_BANAT	Q52w83 bangia atro
1163	57	12.4	342	1	ISIA_SINP6	Q5n575 synchococc
1164	57	12.4	342	1	ISIA_SINP7	Fl5347 synchococc
1165	57	12.4	342	2	Q31MZ7_SINP7	Q31mz7 synchococc
1166	57	12.4	343	2	Q5LM56_SILPO	Q5lm56 silicibacte
1167	57	12.4	351	2	Q97774_FELCA	Q97774 felis silve
1168	57	12.4	352	2	Q867D6_FELCA	Q867d6 felis silve
1169	57	12.4	353	2	Q9LR37_ATHAT	Q9lr37 arabidopsis
1170	57	12.4	355	2	Q5QNA9_ORYSA	Q5qna9 oryza sativ
1171	57	12.4	360	2	Q8WBK3_GAVES	Q8wbk3 saurothera
1172	57	12.4	372	2	Q2JJC4_9CVAN	Q2jjc4 cyanobacter
1173	57	12.4	374	2	Q80638_ATHAT	Q80638 arabidopsis
1174	57	12.4	374	2	Q672B8_ATHAT	Q672b8 arabidopsis
1175	57	12.4	374	2	Q9SVF3_ATHAT	Q9svf3 arabidopsis
1176	57	12.4	374	2	Q2WCM8_LISMO	Q2wcm8 listeria mo
1177	57	12.4	374	2	Q5NXV2_AZOSE	Q5nxv2 azoarcus sp
1178	57	12.4	376	2	Q6FV38_CANGA	Q6fv38 candida gla
1179	57	12.4	383	2	Q6HGU3_BACHK	Q6hgu3 bacillus th
1180	57	12.4	383	2	Q81NM9_BACAN	Q81nm9 bacillus an
1181	57	12.4	384	2	Q65X10_ORYSA	Q65x10 oryza sativ
1182	57	12.4	385	2	Q9S2G0_ATHAT	Q9s2g0 arabidopsis
1183	57	12.4	386	2	Q5NFP0_FRATT	Q5nfp0 francisella
1184	57	12.4	387	2	Q5B694_EMENI	Q5b694 aspergillus
1185	57	12.4	387	2	Q6AOC8_DESPS	Q6aoc8 desulfotale
1186	57	12.4	394	2	Q47B29_DECAR	Q47b29 dechloromon
1187	57	12.4	399	2	Q53J03_SHIFL	Q53j03 shigella fl
1188	57	12.4	404	2	Q2IMU0_9DELT	Q2imu0 anaeromxob
1189	57	12.4	409	2	Q639H1_BACCC	Q639h1 bacillus ce
1190	57	12.4	425	2	Q2N773_9SPHN	Q2n773 erythroblast
1191	57	12.4	440	2	Q9LMU8_ATHAT	Q9lm8 arabidopsis
1192	57	12.4	440	2	Q8BJG0_MOUSE	Q8bjg0 mus musculus
1193	57	12.4	447	2	Q3Z4H2_SHISS	Q3z4h2 shigella so
1194	57	12.4	456	2	Q97N14_CLOAB	Q97n14 clostridium
1195	57	12.4	457	1	PROY_ECOL6	P0aae4 escherichia
1196	57	12.4	457	1	PROY_ECOL6	P0aae3 escherichia
1197	57	12.4	457	1	PROY_ECOL1	P0aae2 escherichia
1198	57	12.4	457	2	Q3Z507_SHISS	Q3z507 shigella so
1199	57	12.4	457	2	Q2MC24_ECOL1	Q2mc24 escherichia

Q325j8	shigella bo	1200	57	12.4	457	2	Q325J8_SHIBS	Q325j8 shigella bo
Q32if4	shigella dy	1201	57	12.4	457	2	Q32JF4_SHIDS	Q32if4 shigella dy
Q83eg9	shigella fl	1202	57	12.4	457	2	Q83SG9_SHIFL	Q83eg9 shigella fl
P0abp4	escherichia	1203	57	12.4	461	1	DCUC_ECOL5	P0abp4 escherichia
P0abp3	escherichia	1204	57	12.4	461	1	DCUC_ECOL6	P0abp3 escherichia
P0abp5	shigella fl	1205	57	12.4	461	1	DCUC_SHIFL	P0abp5 shigella fl
Q2t4w0	burkholderi	1206	57	12.4	461	1	Q2T4W0_BURTH	Q2t4w0 burkholderi
Q324s1	shigella bo	1207	57	12.4	461	2	Q324S1_SHIBS	Q324s1 shigella bo
Q395s6	burkholderi	1208	57	12.4	461	2	Q395S6_BURS3	Q395s6 burkholderi
Q3Jfv9	burkholderi	1209	57	12.4	461	2	Q3JFV9_BURP1	Q3Jfv9 burkholderi
Q57ru8	salmonella	1210	57	12.4	461	2	Q57RUE8_SALCH	Q57ru8 salmonella
Q63m54	burkholderi	1211	57	12.4	461	2	Q63M54_BURPS	Q63m54 burkholderi
Q7qd04	anopheles g	1212	57	12.4	468	2	Q7QD04_ANOGA	Q7qd04 anopheles g
Q34ae3	pelobacter	1213	57	12.4	470	2	Q34AE3_PELCD	Q34ae3 pelobacter
Q5Jnb5	oryza sativ	1214	57	12.4	471	2	Q5JNB5_ORYSA	Q5Jnb5 oryza sativ
Q83TQ3	listeria mo	1215	57	12.4	471	2	Q83TQ3_LISMO	Q83TQ3 listeria mo
Q84dp6	listeria mo	1216	57	12.4	477	2	Q84DP6_LISMO	Q84dp6 listeria mo
Q84dp7	listeria mo	1217	57	12.4	477	2	Q84DP7_LISMO	Q84dp7 listeria mo
Q84dp8	listeria mo	1218	57	12.4	477	2	Q84DP8_LISMO	Q84dp8 listeria mo
Q84dp9	listeria mo	1219	57	12.4	477	2	Q84DP9_LISMO	Q84dp9 listeria mo
Q84dq0	listeria mo	1220	57	12.4	477	2	Q84DQ0_LISMO	Q84dq0 listeria mo
Q84dn9	listeria mo	1221	57	12.4	477	2	Q84DN9_LISMO	Q84dn9 listeria mo
Q84dn7	listeria mo	1222	57	12.4	478	2	Q84DS7_LISMO	Q84dn7 listeria mo
Q84ds7	listeria mo	1223	57	12.4	478	2	Q84DS7_LISMO	Q84ds7 listeria mo
Q2K3u6	rhizobium e	1224	57	12.4	479	1	Q2K3U6_RHET	Q2k3u6 rhizobium e
P51356	porphyra pu	1225	57	12.4	487	1	P5B3C_PORPU	P51356 porphyra pu
Q8nhd7	arabidopsis	1226	57	12.4	487	1	Q8NHD7_ATHAT	Q8nhd7 arabidopsis
Q93zu2	arabidopsis	1227	57	12.4	487	2	Q93ZU2_ATHAT	Q93zu2 arabidopsis
Q7nc13	mycoplasma	1228	57	12.4	493	2	Q7NC13_MYCGA	Q7nc13 mycoplasma
Q61vz5	photobacter	1229	57	12.4	494	1	ILVC_PHOPR	Q61vz5 photobacter
Q316v4	nitrosococ	1230	57	12.4	499	2	Q316V4_NITOC	Q316v4 nitrosococ
Q37v73	novosphingo	1231	57	12.4	516	2	Q37V73_SHAR	Q37v73 novosphingo
Q2xm06	pseudomonas	1232	57	12.4	517	2	Q2XM06_PSEPU	Q2xm06 pseudomonas
Q88gw6	pseudomonas	1233	57	12.4	517	2	Q88GW6_PSEPK	Q88gw6 pseudomonas
Q60vx5	caenorhabdi	1234	57	12.4	531	2	Q60VX5_CAEBR	Q60vx5 caenorhabdi
Q4wg10	aspergillus	1235	57	12.4	534	2	Q4WG10_ASPFR	Q4wg10 aspergillus
Q4kir3	pseudomonas	1236	57	12.4	535	2	Q4KIR3_PSEF5	Q4kir3 pseudomonas
Q3sfm7	thiobacillus	1237	57	12.4	551	2	Q3SFM7_THIDA	Q3sfm7 thiobacillus
Q2uba3	aspergillus	1238	57	12.4	555	2	Q2UBA3_ASPOR	Q2uba3 aspergillus
Q88ye8	mus musculus	1239	57	12.4	576	2	Q88YE8_MOUSE	Q88ye8 mus musculus
Q88am8	pseudomonas	1240	57	12.4	606	2	Q88AM8_PSESM	Q88am8 pseudomonas
Q722H9	homo sapien	1241	57	12.4	610	2	Q722H9_HUMAN	Q722h9 homo sapien
Q8n695	homo sapien	1242	57	12.4	610	2	Q8N695_HUMAN	Q8n695 homo sapien
Q2tb99	homo sapien	1243	57	12.4	610	2	Q2TB99_HUMAN	Q2tb99 homo sapien
Q413y7	gibberella	1244	57	12.4	629	2	Q413Y7_GBIZE	Q413y7 gibberella
Q746h7	thermus the	1245	57	12.4	633	2	Q746H7_THET2	Q746h7 thermus the
Q8mjd4	oryctolagus	1246	57	12.4	641	2	Q8MJD4_RABIT	Q8mjd4 oryctolagus
Q2kb68	rhizobium e	1247	57	12.4	661	2	Q2KB68_RHET	Q2kb68 rhizobium e
Q40qil	desulfurom	1248	57	12.4	679	2	Q40QI1_DESAC	Q40qil desulfurom
Q64i8	butyrivibri	1249	57	12.4	689	2	Q64I8_BUTFI	Q64i8 butyrivibri
Q7nii1	gloeobacter	1250	57	12.4	699	2	Q7NII1_GLOVI	Q7nii1 gloeobacter
Q4fxz2	leishmania	1251	57	12.4	811	2	Q4FXZ2_LEIMA	Q4fxz2 leishmania
Q6zpe7	mus musculus	1252	57	12.4	858	2	Q6ZPE7_MOUSE	Q6zpe7 mus musculus
Q6ki07	mycoplasma	1253	57	12.4	880	2	Q6KI07_MYCMO	Q6ki07 mycoplasma
Q5lum8	silicibacte	1254	57	12.4	892	2	Q5LUM8_SILPO	Q5lum8 silicibacte
Q9rlc7	mus musculus	1255	57	12.4	953	1	PRF40_MOUSE	Q9rlc7 mus musculus
Q2p227	xanthomonas	1256	57	12.4	1056	2	Q2P227_XANOR	Q2p227 xanthomonas
Q5gr12	xanthomonas	1262	57	12.4	1056	2	Q5GZ12_XANOR	Q5gr12 xanthomonas
Q2w307	magnetospir	1263	57	12.4	1068	2	Q2W307_MAGSA	Q2w307 magnetospir
Q82e10	streptomyce	1264	57	12.4	1137	2	Q82E10_STRAW	Q82e10 streptomyce
Q2qk19	brachydanio	1265	57	12.4	1141	2	Q2QK19_BRARE	Q2qk19 brachydanio
Q754s3	ashbya goss	1266	57	12.4	1151	2	Q754S3_ASHGO	Q754s3 ashbya goss
Q3qc38	shewanella	1267	57	12.4	1185	2	Q3QC38_9GAMM	Q3qc38 shewanella
Q443x7	solibacter	1268	57	12.4	1213	2	Q443X7_SOIUS	Q443x7 solibacter
Q50hm7	streptomyce	1269	57	12.4	1294	2	Q50HM7_STESH	Q50hm7 streptomyce
Q5gf21	haemophilus	1270	57	12.4	1491	2	Q5GF21_HABIN	Q5gf21 haemophilus
Q2nph0	xanthomonas	1271	57	12.4	1571	2	Q2NPH0_9CAUD	Q2nph0 xanthomonas
		1272	57	12.4				



835	58.5	12.7	482	2	Q97CF4	THEVO	Q97cf4	thermoplas	908	58	12.6	331	2	Q65F35	BACLD	Q65f35	bacillus li
836	58.5	12.7	492	2	Q2UR56	ASPOR	Q2ur56	aspergillus	909	58	12.6	333	2	Q8N7W6	HUMAN	Q8n7w6	homo sapien
837	58.5	12.7	499	2	Q4NDZ1	9MICC	Q4ndz1	arthrobacte	910	58	12.6	338	2	Q3GNL5	9GAMM	Q3gnl5	psychobact
838	58.5	12.7	509	2	Q5NSN5	9TRYP	Q5nsn5	trypanosoma	911	58	12.6	338	2	Q2VRR2	ANAPL	Q2vrr2	anas platyr
839	58.5	12.7	516	2	Q84DM1	LISSE	Q84dm1	listeria se	912	58	12.6	344	2	Q4V1K5	BACCZ	Q4v1k5	bacillus ce
840	58.5	12.7	516	2	Q84DU3	LISSE	Q84du3	listeria se	913	58	12.6	344	2	Q6AXV5	RAT	Q6axv5	rattus norv
841	58.5	12.7	557	2	Q8VZE2	ARATH	Q8vze2	arabidopsis	914	58	12.6	345	1	ARGC	BACAN	Q8lmg5	bacillus an
842	58.5	12.7	565	2	Q83DB5	COXBH	Q83db5	coxiella bu	915	58	12.6	349	2	Q7MGC8	VIBVY	Q7mgc8	vibrio vuln
843	58.5	12.7	570	2	Q3WTT0	9RHIZ	Q3wtt0	mesorhizobi	916	58	12.6	354	2	Q95HB3	ANAPL	Q95hb3	anas platyr
844	58.5	12.7	586	2	Q2IZ98	RHOPEU	Q2iz98	rhodopseudo	917	58	12.6	368	2	Q23311	CAEEL	Q23311	caenorhabdi
845	58.5	12.7	587	2	Q46RL3	RALEJ	Q46rl3	ralstonia e	918	58	12.6	369	2	Q3CML7	ALUTAT	Q3cm17	pseudocalt
846	58.5	12.7	587	2	Q91A29	ONCWF	Q91a29	oncorhynch	919	58	12.6	376	2	Q3W5W5	9ACTO	Q3w5w5	frankia sp.
847	58.5	12.7	615	2	Q3GQAL	9GAMM	Q3gqal	psychobact	920	58	12.6	369	2	Q926X9	LISIN	Q926x9	listeria in
848	58.5	12.7	633	2	Q9LMH4	ARATH	Q9lmh4	arabidopsis	921	58	12.6	383	2	Q81BN5	BACCR	Q81bn5	bacillus ce
849	58.5	12.7	639	2	Q4HWW9	GIBZE	Q4hww9	gibberella	922	58	12.6	387	2	Q3KQZ5	MOUSE	Q3kqz5	mus muscul
850	58.5	12.7	652	2	Q6VWT8	NPVCD	Q6vwt8	choristoneu	923	58	12.6	390	2	Q3EJR8	BACTI	Q3ejr8	bacillus th
851	58.5	12.7	679	2	Q4C8Q3	CROWT	Q4c8q3	cryptospori	924	58	12.6	395	2	Q7PSF3	ANOGA	Q7psf3	anopheles g
852	58.5	12.7	683	2	Q5CN79	CRYHO	Q5cn79	crotylospor	925	58	12.6	398	1	SELI	MOUSE	Q80tal	mus muscul
853	58.5	12.7	685	2	Q367G1	9GAMM	Q367g1	shewanella	926	58	12.6	398	2	Q9KPH1	VIBCH	Q9kph1	vibrio chol
854	58.5	12.7	716	2	Q53UCB	WHEAT	Q53ucb	tritricum ae	927	58	12.6	403	2	Q5F7W0	NEIGI	Q5f7w0	neisseria g
855	58.5	12.7	716	2	Q58QF6	WHEAT	Q58qf6	tritricum ae	928	58	12.6	409	2	Q4MX56	BACCE	Q4mx56	bacillus ce
856	58.5	12.7	719	2	Q89QF6	WHEAT	Q89qf6	bacteroides	929	58	12.6	411	2	Q7YQP7	OCNPR	Q7yqp7	ochotona pr
857	58.5	12.7	726	2	Q89TN2	9MAGN	Q89tn2	ramanzania	930	58	12.6	425	2	Q3C7K5	9CLOT	Q3c7k5	peleodictyon
858	58.5	12.7	731	2	Q37R00	SPHAR	Q37r00	novosphingo	931	58	12.6	429	2	Q3B2J5	PELLO	Q3b2j5	pelodictyon
859	58.5	12.7	733	2	Q3NN16	SHEFR	Q3nn16	shewanella	932	58	12.6	440	2	Q4MSY3	BACCE	Q4msy3	bacillus ce
860	58.5	12.7	807	2	Q380A5	SPHAR	Q380a5	novosphingo	933	58	12.6	440	2	Q63DG6	BACCZ	Q63dg6	bacillus ce
861	58.5	12.7	818	2	Q3PK62	PARDE	Q3pk62	paracoccus	934	58	12.6	440	2	Q6HKY9	BACHK	Q6hky9	bacillus th
862	58.5	12.7	876	1	SYL	NEIMB	Q3pk62	paracoccus	935	58	12.6	440	2	Q81FL1	BACCR	Q81fl1	bacillus ce
863	58.5	12.7	878	2	Q5FAJ3	NEIGI	Q5faj3	neisseria m	936	58	12.6	440	2	Q81SQ4	BACAN	Q81sq4	bacillus an
864	58.5	12.7	1048	2	Q6EMD9	ECOLI	Q6emd9	escherichia	937	58	12.6	440	2	Q73AS4	BACCI	Q73as4	bacillus ce
865	58.5	12.7	1048	2	Q6UEN9	KLEPN	Q6uen9	klebsiella	938	58	12.6	444	2	Q4SMG6	TITNG	Q4smg6	tetractodon
866	58.5	12.7	1105	2	Q9CFH5	ARATH	Q9cfh5	arabidopsis	939	58	12.6	448	2	Q84DP2	LISMO	Q84dp2	listeria mo
867	58.5	12.7	1105	2	Q5F3N7	CHICK	Q5f3n7	gallus gall	940	58	12.6	457	2	Q4KJP7	PSEFS	Q4kjp7	pseudomonas
868	58.5	12.7	1140	2	Q33RL7	9GAMM	Q33rl7	shewanella	941	58	12.6	461	2	Q8ZR07	SALTY	Q8zr07	salmonella
869	58.5	12.7	1189	2	Q44415	9RHIZ	Q44415	agrobacteri	942	58	12.6	462	2	Q9RYH5	DEIRA	Q9ryh5	deinococcus
870	58.5	12.7	1720	2	Q4FXS8	LEIMA	Q4fxs8	leishmania	943	58	12.6	486	2	Q6DBW3	BRARE	Q6dbw3	brachydanio
871	58.5	12.7	1817	2	Q7SZF6	XENLA	Q7szf6	xenopus lae	944	58	12.6	487	2	Q4T7M0	TITNG	Q4t7m0	tetractodon
872	58.5	12.7	2473	2	Q9SLC7	9MAMM	Q9slc7	tachyglossu	945	58	12.6	511	2	Q74CB3	GEOSL	Q74cb3	geobacter s
873	58.5	12.7	2710	2	Q8T3G9	CAEEL	Q8t3g9	caenorhabdi	946	58	12.6	541	2	Q21L02	9BELT	Q21l02	anaeromyxob
874	58.5	12.7	2712	2	Q01808	CAEEL	Q01808	caenorhabdi	947	58	12.6	548	2	Q2T1P3	BURTH	Q2t1p3	burkholderi
875	58.5	12.7	5359	2	Q5VKR4	SACER	Q5vkr4	saccharopol	948	58	12.6	548	2	Q4DK73	TRYCR	Q4dk73	trypanosoma
876	58.5	12.7	6193	2	Q8K5Q0	STRCP	Q8k5q0	streptomyce	949	58	12.6	549	2	Q4DSC2	TRYCR	Q4dsc2	trypanosoma
877	58	12.6	89	2	Q3SPX3	NITWN	Q3spx3	nitrobacter	950	58	12.6	549	2	Q8GGR2	STRAZ	Q8ggr2	streptomyce
878	58	12.6	96	2	Q83B08	COXBU	Q83b08	coxiella bu	951	58	12.6	549	2	Q8GGR2	STRAZ	Q8ggr2	streptomyce
879	58	12.6	104	2	Q24949	FASHE	Q24949	fasciola he	952	58	12.6	551	2	Q2UPK5	ASPOR	Q2upk5	aspergillus
880	58	12.6	113	2	Q3ULC1	MOUSE	Q3ulc1	mus musculu	953	58	12.6	552	2	Q4J322	AXOVI	Q4j322	azobacter
881	58	12.6	114	1	YDGL	BACSU	P96702	bacillus su	954	58	12.6	553	2	Q942J6	ORYSA	Q942j6	oryza sativ
882	58	12.6	120	2	Q4J5Z8	AZOV1	Q4j5z8	azotobacter	955	58	12.6	614	2	Q7UVX4	RHOBA	Q7uvx4	rhodopirell
883	58	12.6	175	2	Q5WAS8	BACSK	Q5was8	bacillus cl	956	58	12.6	626	2	Q3TS47	MOUSE	Q3ts47	mus musculu
884	58	12.6	177	2	Q9EUW4	LISIN	Q9euw4	listeria in	957	58	12.6	629	2	Q86146	CAMJE	Q86146	campylobact
885	58	12.6	185	2	Q5PCY5	SALPA	Q5pcy5	salmonella	958	58	12.6	662	2	Q3BQJ3	XANCS	Q3bjq3	xanthomonas
886	58	12.6	185	2	Q5PJ65	SALPA	Q5pj65	salmonella	959	58	12.6	674	2	Q8PHZ1	XANAC	Q8phz1	xanthomonas
887	58	12.6	185	2	Q8ZK73	SALTY	Q8zk73	salmonella	960	58	12.6	675	2	Q2P4Y0	XANOR	Q2p4y0	xanthomonas
888	58	12.6	185	2	Q8Z152	SALTY	Q8z152	salmonella	961	58	12.6	675	2	Q5H226	XANOR	Q5h226	xanthomonas
889	58	12.6	196	2	Q9RYZ1	DEIRA	Q9ryz1	deinococcus	962	58	12.6	676	2	Q8XQP3	RALSO	Q8xqp3	ralstonia s
890	58	12.6	215	2	Q57NR2	SALCH	Q57nr2	salmonella	963	58	12.6	681	1	GAZL1	HUMAN	Q95f01	homo sapien
891	58	12.6	215	2	Q5PCY5	SALPA	Q5pcy5	salmonella	964	58	12.6	682	2	Q4HU14	GIBZE	Q4hu14	gibberella
892	58	12.6	215	2	Q7CQF4	SALTY	Q7cqf4	salmonella	965	58	12.6	695	2	Q4HLX6	CAMLA	Q4hlx6	campylobact
893	58	12.6	232	2	Q8XF20	SALTY	Q8xf20	salmonella	966	58	12.6	743	2	Q6FJV9	CANGA	Q6fjv9	candida gla
894	58	12.6	232	2	Q5EQQ0	VIBF1	Q5eqq0	vibrio fisc	967	58	12.6	758	2	Q9VQW0	DROME	Q9vqw0	drosophila
895	58	12.6	253	2	Q2LSR3	9DELT	Q2lsr3	syntriphos	968	58	12.6	767	2	Q51CV0	ENTHI	Q51cv0	entamoeba h
896	58	12.6	253	2	Q3PMW2	NITHA	Q3pmw2	nitrobacter	969	58	12.6	778	2	Q6OZP1	CAEBR	Q6ozp1	caenorhabdi
897	58	12.6	257	1	DPHB	METJA	Q58670	methanococ	970	58	12.6	808	2	Q37XW6	SPHAR	Q37xw6	novosphingo
898	58	12.6	263	2	Q9FP64	ORYSA	Q9fp64	oryza sativ	971	58	12.6	876	2	Q31593	XENLA	Q31593	xenopus lae
899	58	12.6	277	1	RAFR	PEDE	Q43465	pediococcus	972	58	12.6	978	2	Q5BDP3	EMENI	Q5bdp3	aspergillus
900	58	12.6	281	2	Q4B1K8	9URPK	Q4b1k8	polaromonas	973	58	12.6	1006	2	Q4NI49	9MTC	Q4ni49	arthrobacte
901	58	12.6	283	2	Q37HA7	RHOPE	Q37ha7	rhodopseudo	974	58	12.6	1018	2	Q6ALX0	DESFS	Q6alx0	desulfotale
902	58	12.6	289	2	Q419J6	KINRA	Q419j6	kineococcus	975	58	12.6	1044	2	Q47D66	DECAR	Q47d66	dechloromon
903	58	12.6	314	2	Q6IK08	DROME	Q6ik08	drosophila	976	58	12.6	1051	2	Q5B9V4	EMENI	Q5b9v4	aspergillus
904	58	12.6	316	2	Q46SU8	RALEJ	Q46su8	ralstonia e	977	58	12.6	1056	2	Q7S8Q2	NEUCR	Q7s8q2	neurospora
905	58	12.6	322	2	Q3WKT7	9RHIZ	Q3wkt7	mesorhizobi	978	58	12.6	1056	2	Q3BS55	XANCS	Q3bs55	xanthomonas
906	58	12.6	325	2	Q9ELT9	9VIRU	Q9elt9	rice grassy	979	58	12.6	1056	2	Q8FJN1	XANAC	Q8fjn1	xanthomonas
907	58	12.6	326	2	Q2VR11	ANAPL	Q2vr11	anas platyr	980	58	12.6	1109	2	Q7JR52	DROME	Q7jr52	drosophila

689	59	12.8	293	2	Q2ZX54_SHEPU	Q2zx54 shewanella	762	59	12.8	898	2	Q91592_XENLA	Q91592 xenopus lae
690	59	12.8	306	2	Q3GK95_9FIRM	Q3gk95 syntrophomo	763	59	12.8	907	1	KCNB2_RAT	Q63099 rattus norv
691	59	12.8	310	2	Q37D92_RHOPA	Q37d92 rhodopseuo	764	59	12.8	911	1	KCNB2_HUMAN	Q92953 homo sapien
692	59	12.8	310	2	Q9A410_CAUCR	Q9a410 caulobacter	765	59	12.8	911	1	KCNB2_RABIT	Q95111 oryctolagus
693	59	12.8	312	2	Q2J2C5_RHOPA	Q2j2c5 rhodopseuo	766	59	12.8	911	2	Q7Z7D0_HUMAN	Q7z7d0 homo sapien
694	59	12.8	316	2	Q577P4_BRUAB	Q577p4 brucella ab	767	59	12.8	911	2	Q4ZHA6_BOVIN	Q4zha6 bos taurus
695	59	12.8	326	2	Q8FWG7_BRUSU	Q8fwg7 brucella su	768	59	12.8	936	2	Q6GNW5_XENLA	Q6gnw5 xenopus lae
696	59	12.8	326	2	Q8YBV7_BRUME	Q8ybv7 brucella me	769	59	12.8	971	2	Q5AXB1_ENENI	Q5axb1 aspergillus
697	59	12.8	326	2	Q2YKB4_BRUA2	Q2ykb4 brucella ab	770	59	12.8	1027	2	Q488L9_COLP3	Q488l9 colwellia p
698	59	12.8	333	2	Q46SW4_RALEJ	Q46sw4 ralstonia e	771	59	12.8	1078	2	Q4ISZ0_AZOV1	Q4iszo azotobacter
699	59	12.8	338	2	Q2VRR1_ANAPL	Q2vrr1 anas platyr	772	59	12.8	1211	2	Q57WZ8_9TRYP	Q57wz8 trypanosoma
700	59	12.8	340	2	Q3MBT7_ANAV1	Q3mbt7 anabaena va	773	59	12.8	1263	2	Q4P3P5_USTMA	Q4p3p5 ustilago ma
701	59	12.8	345	1	ARC8_BACHK	Q6he28 bacillus th	774	58.5	12.7	1426	2	Q36NM6_MARHY	Q36nm6 marinobacte
702	59	12.8	345	2	Q635F0_BACZC	Q635f0 bacillus ce	775	58.5	12.7	133	2	Q8DA24_VIBVU	Q8da24 vibrio vuln
703	59	12.8	350	2	Q7MQV1_WOLSU	Q7mqv1 wolinnella s	776	58.5	12.7	153	2	Q7MK55_VIBVY	Q7mk55 vibrio vuln
704	59	12.8	356	2	Q7XJY8_ORYSA	Q7xjy8 oryza sativ	777	58.5	12.7	156	2	Q3BQX7_XANCS	Q3bqx7 xanthomonas
705	59	12.8	361	2	Q46SQ0_RALEJ	Q46sq0 ralstonia e	778	58.5	12.7	161	2	Q3S1M0_CAEEL	Q3s1m0 caenorhabdi
706	59	12.8	363	2	Q3RU05_RALME	Q3ru05 ralstonia m	779	58.5	12.7	169	2	Q6MLM7_BDEBA	Q6mlm7 bdellovibri
707	59	12.8	369	2	Q7QZG4_GIALA	Q7qzg4 giardia lam	780	58.5	12.7	182	2	Q916C9_PSEAE	Q916c9 pseudomonas
708	59	12.8	370	2	Q98F86_RHILIO	Q98f86 rhizobium l	781	58.5	12.7	189	2	Q852L5_ORYSA	Q852l5 oryza sativ
709	59	12.8	377	2	Q4M20_0DESAC	Q4m20 desulfuromo	782	58.5	12.7	194	2	Q7QBS9_ANGSA	Q7qbs9 anopheles g
710	59	12.8	381	2	Q5OWF6_ENTHI	Q5owf6 entamoeba h	783	58.5	12.7	196	1	CLPP_HELHP	Q7vin7 helicobacte
711	59	12.8	386	2	Q440C5_SOLUS	Q440c5 solibacter	784	58.5	12.7	200	2	Q4TT87_CAEEL	Q4tt87 caenorhabdi
712	59	12.8	419	2	Q97VB7_SULSO	Q97vb7 rhizobium s	785	58.5	12.7	215	2	Q2J2R0_RHOPA	Q2j2r0 rhodopseuo
713	59	12.8	420	2	Q926F0_RHIME	Q926f0 rhizobium m	786	58.5	12.7	217	2	Q96XX6_SULTO	Q96xx6 sulfobus
714	59	12.8	425	2	Q836T8_ENTFA	Q836t8 enterococcu	787	58.5	12.7	221	2	Q4SQX2_TETNG	Q4sqx2 tetraodon n
715	59	12.8	447	2	Q605T5_METCA	Q605t5 methylococc	788	58.5	12.7	222	2	Q7N7R7_PHOLL	Q7n7r7 photorhabdu
716	59	12.8	448	2	Q7NZN0_CHRVO	Q7nzn0 chromobacte	789	58.5	12.7	238	2	Q4SDB4_TETNG	Q4sdb4 tetraodon n
717	59	12.8	452	2	Q3BPC6_XANCS	Q3bpc6 xanthomonas	790	58.5	12.7	239	2	Q66IB5_BRARE	Q66ib5 brachydanio
718	59	12.8	463	2	Q6PC35_BRARE	Q6pc35 brachydanio	791	58.5	12.7	260	1	NRPN_HUMAN	Q60259 homo sapien
719	59	12.8	463	2	Q8JHG2_BRARE	Q8jhg2 brachydanio	792	58.5	12.7	260	2	Q81W69_HUMAN	Q81w69 homo sapien
720	59	12.8	479	1	NUON2_RHIME	P56911 rhizobium m	793	58.5	12.7	260	2	Q88YT6_LACPL	Q88yt6 lactobacill
721	59	12.8	489	2	Q316W8_DESDG	Q316w8 desulfovibr	794	58.5	12.7	265	2	Q603A7_METCA	Q603a7 methylococc
722	59	12.8	490	2	Q2JPR9_9CYAN	Q2jpr9 cyanobacter	795	58.5	12.7	268	2	Q3GQC6_9GAMM	Q3gqc6 psychrobact
723	59	12.8	502	2	Q2KU57_BORAV	Q2ku57 bordetella	796	58.5	12.7	277	2	Q3Y2T3_ENTFC	Q3y2t3 enterococcu
724	59	12.8	526	2	Q6X1D5_9RHAB	Q6x1d5 aravan viru	797	58.5	12.7	299	2	Q7NWJ4_CHRVO	Q7nwj4 chromobacte
725	59	12.8	543	2	Q2T6B0_BURTH	Q2t6b0 burkholderi	798	58.5	12.7	299	2	Q7W0P0_BORPE	Q7w0p0 bordetella
726	59	12.8	545	2	Q3HHA2_TRIER	Q3hha2 trichodesmi	799	58.5	12.7	299	2	Q7W3G6_BORPA	Q7w3g6 bordetella
727	59	12.8	552	2	Q41BY1_GIBZE	Q41by1 gibberella	800	58.5	12.7	299	2	Q7WET6_BORBE	Q7wet6 bordetella
728	59	12.8	557	2	Q5R7Q0_PONPY	Q5r7q0 pongo pygma	801	58.5	12.7	303	2	Q5XVK9_ARATH	Q5xvk9 arabidopsis
729	59	12.8	558	2	Q92C60_LISIN	Q92c60 listeria in	802	58.5	12.7	321	1	TILS_BORPE	Q7vxt7 bordetella
730	59	12.8	575	2	Q9QUU4_9MURI	Q9quu4 rattus sp.	803	58.5	12.7	326	2	Q3WTT7_9RHIZ	Q3wtt7 mesorhizobi
731	59	12.8	579	2	Q6U666_KLEPN	Q6u666 klebsiella	804	58.5	12.7	328	2	Q6LEX6_PLAF7	Q6lex6 plasmodium
732	59	12.8	598	2	Q4SURO_TETNG	Q4suro tetraodon n	805	58.5	12.7	336	2	Q828R5_STRAM	Q828r5 streptomyce
733	59	12.8	611	2	Q8WNQ3_PIG	Q8wnq3 sus scrofa	806	58.5	12.7	340	2	Q8R782_THETN	Q8r782 thermoanaer
734	59	12.8	623	2	Q53W46_THET8	Q53w46 thermus the	807	58.5	12.7	341	2	Q3FBN1_9BURK	Q3fbn1 burkholderi
735	59	12.8	653	2	Q5REB6_PONPY	Q5reb6 pongo pygma	808	58.5	12.7	344	2	Q4NGO6_9MICC	Q4ng06 arthrobacte
736	59	12.8	654	1	KCNM4_MOUSE	Q61423 mus musculu	809	58.5	12.7	347	2	Q47LN7_THEFY	Q47ln7 thermobifid
737	59	12.8	654	2	KCNM4_MUSPF	Q28527 mustela put	810	58.5	12.7	351	2	Q3HBA5_TRIER	Q3hba5 trichodesmi
738	59	12.8	654	2	Q8CBF8_MOUSE	Q8cbf8 m 16 days n	811	58.5	12.7	352	1	CCR5_CANPA	Q5ecr9 canis famil
739	59	12.8	655	1	KCNM4_RAT	P15385 rattus norv	812	58.5	12.7	356	2	Q44HS5_CHRSL	Q44hs5 chromohalob
740	59	12.8	660	1	KCNM4_BOVIN	Q05037 bos taurus	813	58.5	12.7	359	2	Q5L5F2_CHLAB	Q5l5f2 chlamydophi
741	59	12.8	660	2	Q84MG6_ORYSA	Q84mg6 oryza sativ	814	58.5	12.7	362	2	Q99RR9_BRAJA	Q99rr9 bradyrhizob
742	59	12.8	661	2	Q9GLF1_BOVIN	Q9glf1 bos taurus	815	58.5	12.7	366	2	Q22K74_CALSA	Q22k74 caldicellul
743	59	12.8	662	2	Q9W3K6_COLL1	Q9w3k6 collumba liv	816	58.5	12.7	372	2	Q8SGX1_9SAUR	Q8sgx1 pareas macu
744	59	12.8	662	2	Q9YGX8_CHICK	Q9ygx8 gallus gall	817	58.5	12.7	383	1	FAD6E_ARATH	P48133 arabidopsis
745	59	12.8	663	2	Q61VQ2_CAEER	Q61vq2 caenorhabdi	818	58.5	12.7	383	2	Q8LFZ8_ARATH	Q8lfz8 arabidopsis
746	59	12.8	673	2	Q3WBA7_9ACTO	Q3wba7 frankia sp.	819	58.5	12.7	384	2	Q8UAR7_AGRTS	Q8uar7 agrobacteri
747	59	12.8	677	2	Q388H5_9TRYP	Q388h5 trypanosoma	820	58.5	12.7	385	2	Q6ZLL9_ORYSA	Q6zll9 oryza sativ
748	59	12.8	697	2	Q8JG57_XENLA	Q8jg57 xenopus lae	821	58.5	12.7	389	2	Q7CS44_AGRTS	Q7cs44 agrobacteri
749	59	12.8	700	2	Q584E7_PONPY	Q584e7 pongo pygma	822	58.5	12.7	392	2	Q6C9T8_YARLI	Q6c9t8 yarrowia li
750	59	12.8	771	2	Q80X33_MOUSE	Q80x33 mus musculu	823	58.5	12.7	400	1	ERTU_HERAU	P42477 herpetosiph
751	59	12.8	782	2	Q6LKY8_PHOPR	Q6lky8 photobacter	824	58.5	12.7	409	2	Q8DBZ6_VIBVU	Q8dbz6 vibrio vuln
752	59	12.8	787	2	Q5SMW7_ORYSA	Q5smw7 oryza sativ	825	58.5	12.7	411	2	Q9RU03_DEIRA	Q9ru03 deinococcus
753	59	12.8	813	2	Q2NLD5_HUMAN	Q2nld5 homo sapien	826	58.5	12.7	415	2	Q3CN28_ALTAT	Q3cn28 pseudoaalter
754	59	12.8	816	2	Q98SV4_ICTPU	Q98sv4 ictalurus p	827	58.5	12.7	421	2	Q22600_9GAMM	Q22600 shewanella
755	59	12.8	855	2	Q7NET0_MYCGA	Q7net0 mycoplasma	828	58.5	12.7	425	1	YOSB_SCHPO	Q9p7l2 schizosacch
756	59	12.8	857	1	KCNB1_MOUSE	Q03717 mus musculu	829	58.5	12.7	426	2	Q3JF29_NITOC	Q3jf29 nitrosococc
757	59	12.8	857	1	KCNB1_RAT	P15387 rattus norv	830	58.5	12.7	426	2	Q69513_MYCLE	Q69513 mycobacteri
758	59	12.8	857	2	Q8KOD1_MOUSE	Q8kod1 mus musculu	831	58.5	12.7	444	2	Q4D6T2_TRYCL	Q4d6t2 trypanosoma
759	59	12.8	858	1	KCNB1_HUMAN	Q14721 homo sapien	832	58.5	12.7	463	2	Q9CB73_MYCLE	Q9cb73 mycobacteri
760	59	12.8	858	1	KCNB1_PIG	Q18968 sus scrofa	833	58.5	12.7	468	2	Q2STX5_BURTH	Q2stx5 burkholderi
761	59	12.8	858	1	KCNB1_RABIT	Q9mr19 oryctolagus	834	58.5	12.7	471	2	Q4S1G4_TETNG	Q4s1g4 tetraodon n

543	60	13.0	342	2	Q2L4T2_RAT	Q2L4t2 rattus norv	616	59.5	12.9	524	2	Q2YA78_NITMU	Q2ya78 nitrosospir
544	60	13.0	352	2	Q5DWS5_KARMI	Q5dws5 karlodinium	617	59.5	12.9	526	2	Q7VI06_HELHP	Q7vi06 helicobacte
545	60	13.0	365	2	Q69I35_EBVG	Q69i35 epstein-bar	618	59.5	12.9	527	1	TH11_TRYBB	Q06221 trypanosoma
546	60	13.0	369	2	Q6D4F3_ERWCT	Q6d4f3 erwinia car	619	59.5	12.9	527	2	Q26765_9RYP	Q26765 trypanosoma
547	60	13.0	410	2	Q3VHD6_9SPHN	Q3vhd6 sphingopyxi	620	59.5	12.9	528	1	TH12_TRYBB	Q09037 trypanosoma
548	60	13.0	412	2	Q9I3M4_PSEAE	Q9i3m4 pseudomonas	621	59.5	12.9	537	2	Q43S03_SOLUS	Q04303 solibacter
549	60	13.0	470	2	Q404R9_9RHOE	Q404r9 jannaschia	622	59.5	12.9	579	2	Q4EBF6_WORICK	Q4ebf6 wobbachia e
550	60	13.0	497	1	LM22_EBV	Q13285 epstein-bar	623	59.5	12.9	579	2	Q5GTF9_WOLTR	Q5gtf9 wobbachia s
551	60	13.0	497	2	Q777H4_EBVG	Q777h4 epstein-bar	624	59.5	12.9	579	2	Q73I66_WOLPM	Q73i66 wobbachia p
552	60	13.0	502	2	Q9BGM9_9MAMM	Q9bgm9 tachylosteu	625	59.5	12.9	587	2	Q3HGA2_TRIER	Q3hga2 trichodesmi
553	60	13.0	518	2	Q9XE01_STRVG	Q9xe01 streptomyces	626	59.5	12.9	624	2	Q55X46_CRYNE	Q55x46 cryptococcu
554	60	13.0	519	2	Q82LQ9_STRAW	Q82lq9 streptomyces	627	59.5	12.9	624	2	Q5KMT6_CRYNE	Q5kmt6 cryptococcu
555	60	13.0	524	2	Q7T198_CHICK	Q7t198 gallus gall	628	59.5	12.9	636	2	Q48GV9_PSE14	Q48gv9 pseudomonas
556	60	13.0	525	2	Q83J01_SHIFL	Q83j01 shigella fl	629	59.5	12.9	636	2	Q4ZR96_PSEU2	Q4zr96 pseudomonas
557	60	13.0	538	1	YIEC_ECOLI	P26218 escherichia	630	59.5	12.9	677	2	Q87ZAB_PSESM	Q87zab pseudomonas
558	60	13.0	538	2	Q3VYL2_SHISS	Q3vy12 shigella so	631	59.5	12.9	677	2	Q98TW3_XENLA	Q98tw3 xenopus lae
559	60	13.0	538	2	Q2MK38_ECOLI	Q2mk38 escherichia	632	59.5	12.9	687	2	Q3H9I1_TRIER	Q3h9i1 trichodesmi
560	60	13.0	541	2	Q5KNI3_CRYNE	Q5kni3 cryptococcu	633	59.5	12.9	715	2	Q8PSH8_METMA	Q8ps8 methanosarc
561	60	13.0	555	2	Q8VD01_MOUSE	Q8vd01 mus musculu	634	59.5	12.9	727	2	Q4ANX8_CHL8B	Q4anx8 chlorobium
562	60	13.0	580	2	Q7T195_CHICK	Q7t195 gallus gall	635	59.5	12.9	735	2	Q5E3S0_VIBF1	Q5e3s0 vibrio fisc
563	60	13.0	605	2	Q7NHD8_GLOVI	Q7nhd8 gloeobacter	636	59.5	12.9	752	2	Q3SFU4_THIDA	Q3sfu4 thiobacillu
564	60	13.0	611	2	Q8BYF6_MOUSE	Q8byf6 m o day neo	637	59.5	12.9	767	2	Q3G7T1_9DELT	Q3g7t1 pelobacter
565	60	13.0	616	2	Q581Z5_9TRYP	Q581z5 trypanosoma	638	59.5	12.9	768	2	Q4E426_TYCR	Q4e426 trypanosoma
566	60	13.0	616	2	Q9Y1A2_TRYBB	Q9y1a2 trypanosoma	639	59.5	12.9	778	2	Q4RV23_TETNG	Q4rv23 tetraodon n
567	60	13.0	627	2	Q4LRJ4_FERAC	Q4lrj4 ferriplasma	640	59.5	12.9	786	2	Q2IL98_9DELT	Q2il98 anaeromyxob
568	60	13.0	655	2	Q3WIV3_9ACTO	Q3wiv3 frankia sp.	641	59.5	12.9	841	2	Q8H105_ARATH	Q8h105 arabidopsis
569	60	13.0	738	2	Q3JDI8_NITOC	Q3jdi8 nitrococcu	642	59.5	12.9	847	2	Q8RWY4_ARATH	Q8rwy4 arabidopsis
570	60	13.0	756	2	Q55Z68_CRYNE	Q55z68 cryptococcu	643	59.5	12.9	894	2	Q9SGW2_ARATH	Q9sgw2 arabidopsis
571	60	13.0	793	2	Q94BY0_ARATH	Q94by0 arabidopsis	644	59.5	12.9	940	2	Q8T043_DROME	Q8t043 drosophila
572	60	13.0	801	2	Q4A0U1_9BURK	Q4a0u1 polaromonas	645	59.5	12.9	996	2	Q2XM19_PSEPU	Q2xm19 pseudomonas
573	60	13.0	819	1	US6NL_MOUSE	Q80xc3 mus musculu	646	59.5	12.9	1037	2	Q9VZ53_DROME	Q9vz53 drosophila
574	60	13.0	819	2	Q3U2W3_MOUSE	Q3u2w3 mus musculu	647	59.5	12.9	1082	2	Q43L65_SOLUS	Q43l65 solibacter
575	60	13.0	850	2	Q2MHK9_BRARE	Q2mhk9 brachydanio	648	59.5	12.9	1138	2	Q2371_9VIRU	Q2371 laguna negr
576	60	13.0	876	2	Q4ITT5_AZOVI	Q4itt5 azotobacter	649	59.5	12.9	1326	2	Q4DLK6_TYCR	Q4dlk6 trypanosoma
577	60	13.0	1056	2	Q8P875_XANCP	Q8p875 xanthomonas	650	59.5	12.9	1800	2	Q54PV1_DICDI	Q54pv1 dictyosteli
578	60	13.0	1056	2	Q6B8A0_DEBHA	Q6b8a0 debaryomyces	651	59.5	12.9	1800	2	Q8I7P5_DICDI	Q8i7p5 dictyosteli
579	60	13.0	1157	2	Q4SER6_TETNG	Q4ser6 tetraodon n	652	59.5	12.9	1800	2	Q9GMZ2_PIG	Q9gmz2 sus scrofa
580	60	13.0	3187	2	Q4AC22_CHLRE	Q4ac22 chlamydomon	653	59	12.8	119	2	Q8XBD2_ECO57	Q8xbd2 escherichia
581	60	13.0	4149	2	Q2AC22_CHLRE	Q2ac22 chlamydomon	654	59	12.8	130	2	Q4LBF4_9BACT	Q4lbf4 exigubacte
582	60	13.0	5218	1	HTS1_COCOA	Q01886 cochlilobolu	655	59	12.8	137	2	Q3GDC8_9FIRM	Q3gdc8 syntrophomo
583	59.5	12.9	186	2	Q2U0X4_ASPOR	Q2u0x4 aspergillus	656	59	12.8	149	2	Q88UG2_LACPL	Q88ug2 lactobacill
584	59.5	12.9	209	2	Q5KMN0_CRYPTOC	Q5kmn0 cryptococcu	657	59	12.8	149	2	Q88UG2_LACPL	Q88ug2 lactobacill
585	59.5	12.9	214	2	Q7N459_PHOLL	Q7n459 photorhabdu	658	59	12.8	150	2	Q6D7R0_ERWCT	Q6d7r0 erwinia car
586	59.5	12.9	216	2	Q9GJG8_SALTR	Q9gjg8 salmo trutt	659	59	12.8	155	2	Q923L7_MOUSE	Q923l7 mus musculu
587	59.5	12.9	216	2	Q9GJG9_SALTR	Q9gjg9 salmo trutt	660	59	12.8	165	2	Q3QSP5_9RHOE	Q3qsp5 silicibacte
588	59.5	12.9	216	2	Q9GJH0_SALTR	Q9gjh0 salmo trutt	661	59	12.8	167	2	Q8W9B3_VOMUR	Q8w9b3 vombatus ur
589	59.5	12.9	217	2	Q9GJH3_SALTR	Q9gjh3 salmo trutt	662	59	12.8	169	2	Q744R5_MYCPA	Q744r5 mycobacteri
590	59.5	12.9	217	2	Q9GJH4_SALTR	Q9gjh4 salmo trutt	663	59	12.8	175	2	Q97913_FALPE	Q97913 falco pereg
591	59.5	12.9	217	2	Q9GJH6_SALTR	Q9gjh6 salmo trutt	664	59	12.8	177	2	Q92AM4_LISIN	Q92am4 listeria in
592	59.5	12.9	217	2	Q9GJH7_SALTR	Q9gjh7 salmo trutt	665	59	12.8	189	2	Q6X9K8_SULIS	Q6x9k8 sulfolobus
593	59.5	12.9	223	2	Q6PER5_MOUSE	Q6per5 mus musculu	666	59	12.8	189	2	Q6X9L0_SULIS	Q6x9l0 sulfolobus
594	59.5	12.9	228	2	Q3PPC1_NITHA	Q3ppc1 nitrobacter	667	59	12.8	189	2	Q6X9L1_SULIS	Q6x9l1 sulfolobus
595	59.5	12.9	228	2	Q4RJO4_TETNG	Q4rj04 tetraodon n	668	59	12.8	189	2	Q6X9M0_SULIS	Q6x9m0 sulfolobus
596	59.5	12.9	260	2	Q86AQ7_DICDI	Q86aq7 dictyosteli	669	59	12.8	189	2	Q3WSP0_9RHIZ	Q3wsp0 mesorhizobi
597	59.5	12.9	267	2	Q9CG47_LACLA	Q9cg47 lactococcus	670	59	12.8	215	1	YCHE_ECOLI	Q25743 escherichia
598	59.5	12.9	298	2	Q9KKR2_VIBCH	Q9kk2 vibrio chol	671	59	12.8	215	2	Q31ZT2_SHIBS	Q31zt2 shigella bo
599	59.5	12.9	341	2	Q880A3_PSESM	Q880a3 pseudomonas	672	59	12.8	215	2	Q320V6_SHISS	Q320v6 shigella so
600	59.5	12.9	342	2	Q9G5Z0_9SAUR	Q9g5z0 pseudocalot	673	59	12.8	215	2	Q398G3_BURS3	Q398g3 burkholderi
601	59.5	12.9	348	2	Q8XKM0_CLOPE	Q8xkm0 clostridium	674	59	12.8	215	2	Q8FHX1_ECOL6	Q8fhx1 escherichia
602	59.5	12.9	350	2	Q3E0E4_CHLAU	Q3e0e4 chloroflexu	675	59	12.8	215	2	Q8JRN1_SHIFL	Q8jrn1 shigella fl
603	59.5	12.9	356	2	Q9YMM0_NPVLD	Q9ymm0 lymantria d	676	59	12.8	215	2	Q8XDA5_ECO57	Q8xda5 escherichia
604	59.5	12.9	384	2	Q72DS9_DESVH	Q72ds9 desulfovibr	677	59	12.8	231	2	Q2Z5B0_9GAMM	Q2z5b0 shewanella
605	59.5	12.9	385	2	Q4SSP1_TETNG	Q4ssp1 tetraodon n	678	59	12.8	231	2	Q360K8_9GAMM	Q360k8 shewanella
606	59.5	12.9	396	2	Q9U3R3_CAEEL	Q9u3r3 caenorhabdi	679	59	12.8	255	2	Q36DZ6_9GAMM	Q36dz6 burkholderi
607	59.5	12.9	397	2	Q8XSK5_RALSO	Q8xsk5 ralstonia s	680	59	12.8	262	2	Q3FB45_9BURK	Q3fb45 burkholderi
608	59.5	12.9	411	2	Q3SES6_BERAD	Q3ses6 bradyrhizob	681	59	12.8	262	2	Q4XRU0_9PROT	Q4xru0 magnetococc
609	59.5	12.9	421	2	Q2ZU62_SHEPU	Q2zu62 shewanella	682	59	12.8	276	2	Q47F87_DECAR	Q47f87 dechloromon
610	59.5	12.9	426	2	Q6FJK9_CANGA	Q6fjk9 candida gla	683	59	12.8	284	2	Q594H3_9SPHN	Q594h3 agrobacteri
611	59.5	12.9	431	2	Q7XTD3_ORYSA	Q7xtd3 oryza sativ	684	59	12.8	293	1	PUR7_BORBR	Q7wm11 bordetella
612	59.5	12.9	459	2	Q3GU76_9ACTO	Q3gu76 nocardioid	685	59	12.8	293	1	PUR7_BORPA	Q7wb15 bordetella
613	59.5	12.9	467	2	Q2LYB0_9DELT	Q2lyb0 syntrophus	686	59	12.8	293	1	PUR7_BORPE	Q7vy42 bordetella
614	59.5	12.9	467	2	Q2KYV5_BORAV	Q2kyv5 bordetella	687	59	12.8	293	1	PUR7_BORPE	Q7vy42 bordetella
615	59.5	12.9	481	2	Q4E742_9RICK	Q4e742 wobbachia e	688	59	12.8	293	2	Q2X418_9GAMM	Q2x418 shewanella

397	61	13.2	438	2	Q3AW34_SYNS9	Q3aw34	synchococc	470	60.5	13.1	658	2	Q7V8R1_PROMM	Q7v8r1	prochloroco
398	61	13.2	447	2	Q37Q12_SPHAR	Q37q12	novosphingo	471	60.5	13.1	685	2	Q2WWT4_9GAMM	Q2wwt4	shewanella
399	61	13.2	452	2	Q2P0F6_XANOR	Q2p0f6	xanthomonas	472	60.5	13.1	685	2	Q2Z423_9GAMM	Q2z423	shewanella
400	61	13.2	461	2	Q7ACQ0_ECO57	Q7acq0	escherichia	473	60.5	13.1	685	2	Q2ZP33_SHEPU	Q2zp33	shewanella
401	61	13.2	461	2	Q9S5F6_ECOLI	Q9s5f6	escherichia	474	60.5	13.1	726	2	Q35TT5_9GAMM	Q35tt5	shewanella
402	61	13.2	463	2	Q59471_PYROHO	Q59471	pyrococcus	475	60.5	13.1	726	2	Q4HSU4_CAMUP	Q4hsu4	campylobact
403	61	13.2	463	2	Q9V1R1_PYRAB	Q9v1r1	pyrococcus	476	60.5	13.1	728	1	PURL_CAMJE	Q9pny0	campylobact
404	61	13.2	463	2	Q85337_ECOLI	Q85337	escherichia	477	60.5	13.1	728	1	PURL_CAMJE	Q5huk4	campylobact
405	61	13.2	463	2	Q7DBP7_ECO57	Q7dbf2	escherichia	478	60.5	13.1	728	2	Q4HIH9_CAMCO	Q4hih9	campylobact
406	61	13.2	484	2	Q5GXAI_XANOR	Q5gxai	xanthomonas	479	60.5	13.1	742	2	Q9Q0S7_9NFA	Q9nt42	chromobacte
407	61	13.2	488	2	Q521J6_NOCFA	Q521j6	nocardia fa	480	60.5	13.1	776	2	Q7NT42_CHRVO	Q7nt42	chromobacte
408	61	13.2	502	2	Q5DAP6_SCHJA	Q5dap6	schistosoma	481	60.5	13.1	786	2	Q2S1W1_9SPHI	Q2s1w1	salinibacte
409	61	13.2	520	2	Q9SHZ3_ARATH	Q9shz3	arabidopsis	482	60.5	13.1	878	2	Q35UA3_9GAMM	Q35ua3	shewanella
410	61	13.2	542	2	Q5YVG0_NOCFA	Q5yvg0	nocardia fa	483	60.5	13.1	917	2	Q75V17_STAWA	Q75v17	staphylococ
411	61	13.2	568	2	Q61FR3_CABER	Q61fr3	caenothabdi	484	60.5	13.1	1038	2	Q7PPW7_ANGOA	Q7ppw7	anopheles g
412	61	13.2	570	2	Q386Y4_TRYPR	Q386y4	trypanosoma	485	60.5	13.1	1155	2	Q4IU17_AGOVI	Q4iu17	azotobacter
413	61	13.2	638	2	Q6MLY6_DBEBA	Q6mly6	belliovibri	486	60.5	13.1	1227	2	Q2SGL1_9GAMM	Q2sgl1	hahella che
414	61	13.2	651	2	Q9DDN7_9TELE	Q9ddn7	apteronotus	487	60.5	13.1	1285	2	Q2PWA0_9REOV	Q2pwa0	avian ortho
415	61	13.2	653	2	Q73TB8_MYCPA	Q73tb8	mycobacteri	488	60.5	13.1	1285	2	Q5IS12_9REOV	Q5isi2	avian ortho
416	61	13.2	742	2	Q2WNE2_CLOBE	Q2wne2	clostridium	489	60.5	13.1	1285	2	Q5IS13_9REOV	Q5isi3	avian ortho
417	61	13.2	874	2	Q33T29_9GAMM	Q33t29	shewanella	490	60.5	13.1	1285	2	Q5IS14_9REOV	Q5isi4	avian ortho
418	61	13.2	1069	2	Q3P712_PARDE	Q3p712	paracoccus	491	60.5	13.1	1285	2	Q5IS15_9REOV	Q5isi5	avian ortho
419	61	13.2	1305	1	TCGAP_MOUSE	Q80yf9	mus musculus	492	60.5	13.1	1285	2	Q5IS16_9REOV	Q5isi6	avian ortho
420	61	13.2	1324	2	Q3UQS4_MOUSE	Q3uqs4	mus musculus	493	60.5	13.1	1285	2	Q5IS17_9REOV	Q5isi7	avian ortho
421	61	13.2	1526	2	Q5K7V4_CRYNE	Q5k7v4	cryptococcu	494	60.5	13.1	1285	2	Q5IS18_9REOV	Q5isi8	avian ortho
422	61	13.2	1866	2	Q55IB7_CRYNE	Q55ib7	cryptococcu	495	60.5	13.1	1285	2	Q5IS19_9REOV	Q5isi9	avian ortho
423	60.5	13.1	86	2	Q82HNS_STRAW	Q82hns	streptomyce	496	60.5	13.1	1285	2	Q8JUW1_9REOV	Q8juw1	avian reovi
424	60.5	13.1	146	2	Q3FHO1_9BURK	Q3fho1	burkholderi	497	60.5	13.1	1319	2	Q5AYC8_EMENI	Q5ayc8	aspergillus
425	60.5	13.1	163	2	Q5GYF6_XANOR	Q5gyf6	xanthomonas	498	60.5	13.1	1748	2	Q9HGZ5_ASPOR	Q9hgz5	aspergillus
426	60.5	13.1	165	2	Q3B5X3_CHLAU	Q3b5x3	chloroflexu	499	60	13.0	71	1	VITB1_XENLA	P19010	xenopus lae
427	60.5	13.1	166	2	Q2P1G0_XANOR	Q2p1g0	xanthomonas	500	60	13.0	165	2	Q8EPX3_OCEIH	Q8epx3	oceanobacil
428	60.5	13.1	176	2	Q9VUP1_DROME	Q9vup1	drosochila	501	60	13.0	196	2	Q2VL37_9PRIM	Q2vl37	eulemur ful
429	60.5	13.1	210	1	PYRE_BACAN	Q81wf6	bacillus an	502	60	13.0	208	2	Q2VL38_OTOGA	Q2vl38	otolemur ga
430	60.5	13.1	210	1	PYRE_BACCI	Q73217	bacillus ce	503	60	13.0	208	2	Q2VL39_PITPI	Q2vl39	pithecia pi
431	60.5	13.1	210	1	PYRE_BACCH	Q81987	bacillus th	504	60	13.0	208	2	Q2VL40_LAGLA	Q2vl40	lagothrix l
432	60.5	13.1	210	1	PYRE_BACHK	Q6het2	bacillus th	505	60	13.0	208	2	Q2VL41_ATEGE	Q2vl41	ateles geof
433	60.5	13.1	210	1	Q4MJ46_BACCE	Q4mj46	bacillus ce	506	60	13.0	208	2	Q2VL42_COLAN	Q2vl42	colobus ang
434	60.5	13.1	227	2	Q8BX00_ARATH	Q8bx00	arabidopsis	507	60	13.0	208	2	Q2VL43_CERCP	Q2vl43	cercopithec
435	60.5	13.1	241	2	Q3SSH5_NITWN	Q3ssh5	nitrobacter	508	60	13.0	208	2	Q2VL44_PAPAN	Q2vl44	papio anubi
436	60.5	13.1	253	2	Q6W741_PEDICUL	Q6w741	pediculus h	509	60	13.0	208	2	Q2VL45_MANLE	Q2vl45	mandrillus
437	60.5	13.1	279	2	Q3CPP6_ALTAT	Q3cpp6	pseudodalter	510	60	13.0	208	2	Q2VL46_HYLSY	Q2vl46	hylobates s
438	60.5	13.1	286	2	Q417D8_KINRA	Q417d8	kineococcus	511	60	13.0	208	2	Q2VL47_PONSA	Q2vl47	pongo pygma
439	60.5	13.1	289	2	Q7S921_NEUCR	Q7s921	neurospora	512	60	13.0	208	2	Q2VL48_GORGO	Q2vl48	gorilla gor
440	60.5	13.1	295	2	Q22885_ARATH	Q22885	arabidopsis	513	60	13.0	218	2	Q6LT63_PROPR	Q6lt63	photobacter
441	60.5	13.1	306	2	Q21PE9_9DELT	Q21pe9	anaeromyxob	514	60	13.0	218	2	Q8WM93_BRARE	Q8wm93	brachydantio
442	60.5	13.1	312	2	Q9KEQ5_BACCH	Q9keq5	bacillus ha	515	60	13.0	257	2	Q3KXP8_XENLA	Q3kpx8	xenopus lae
443	60.5	13.1	319	2	Q4YCE8_PLABE	Q4yce8	plasmodium	516	60	13.0	275	2	Q8YXA0_ANASP	Q8yxa0	anabaena sp
444	60.5	13.1	326	2	Q97YW6_SULSO	Q97yw6	sulfolobus	517	60	13.0	275	2	Q9VLF8_DROME	Q9vlf8	drosochila
445	60.5	13.1	327	2	Q5XWR0_SOLTU	Q5xwr0	solanum tub	518	60	13.0	277	2	Q4AYA9_9BURK	Q4aya9	polaromonas
446	60.5	13.1	336	2	Q2OCE0_MEGAN	Q2qce0	megadyptes	519	60	13.0	283	2	Q42AB6_DSHA	Q42ab6	desulfitoba
447	60.5	13.1	340	2	Q8LAZ5_ARATH	Q8laz5	arabidopsis	520	60	13.0	288	2	Q88IQ0_PSEPK	Q88iq0	pseudomonas
448	60.5	13.1	354	2	Q9M9T5_ARATH	Q9m9t5	arabidopsis	521	60	13.0	316	2	Q3VWN1_DROME	Q3vwn1	drosochila
449	60.5	13.1	359	2	Q3XNW7_9PROT	Q3xmw7	magnetococc	522	60	13.0	318	2	Q351J2_9GAMM	Q351j2	alkalilimni
450	60.5	13.1	416	2	Q33NX9_9GAMM	Q33nx9	shewanella	523	60	13.0	324	2	Q986J3_RHILO	Q986j3	rhizobium l
451	60.5	13.1	416	2	Q3NX34_9GAMM	Q3nx34	shewanella	524	60	13.0	325	2	Q7XMF8_ORVSA	Q7xmf8	oryza sativ
452	60.5	13.1	427	2	Q9A315_CAUCR	Q9a315	caulobacter	525	60	13.0	341	1	PAX9_CALGO	Q2vl59	callinico g
453	60.5	13.1	434	2	Q4MG72_BACCE	Q4mg72	bacillus ce	526	60	13.0	341	1	PAX9_CALJA	Q2vl58	callithrix
454	60.5	13.1	434	2	Q63AK9_BACCC	Q63ak9	bacillus ce	527	60	13.0	341	1	PAX9_DAUMA	Q2vl53	daubentonia
455	60.5	13.1	434	2	Q81CL5_BACCR	Q81cl5	bacillus ce	528	60	13.0	341	1	PAX9_HUMAN	P55771	homo sapien
456	60.5	13.1	463	2	Q8D167_YERSINIA	Q8d167	yersinia pe	529	60	13.0	341	1	PAX9_LEMCA	Q2vl52	lemur catia
457	60.5	13.1	463	2	Q66DX2_YERPS	Q66dx2	yersinia ps	530	60	13.0	341	1	PAX9_LEORO	Q2vl57	leontopithe
458	60.5	13.1	463	2	Q82C25_YERPE	Q82c25	yersinia pe	531	60	13.0	341	1	PAX9_LEPPD	Q2vl51	lepilemur e
459	60.5	13.1	474	2	Q3J1Z2_BURP1	Q3j1z2	burkholderi	532	60	13.0	341	1	PAX9_MACMU	Q2vl61	macaca mula
460	60.5	13.1	474	2	Q63187_BURPDS	Q63187	burkholderi	533	60	13.0	341	1	PAX9_PANTR	Q2vl62	pan troglod
461	60.5	13.1	478	2	Q86BK5_DROME	Q86bk5	drosochila	534	60	13.0	341	1	PAX9_PERPO	Q2vl54	perodicticu
462	60.5	13.1	484	2	Q4ZBP3_9VIRU	Q4zbp3	bacterioph	535	60	13.0	341	1	PAX9_PANTR	Q2vl50	propithecus
463	60.5	13.1	484	2	Q4ZDK0_9CAUD	Q4zdk0	bacterioph	536	60	13.0	341	1	PAX9_BROVC	Q2vl60	saimiri bol
464	60.5	13.1	484	2	Q6R861_9CAUD	Q6r861	bacterioph	537	60	13.0	341	1	PAX9_SAIIBB	Q2l4tl	homo sapien
465	60.5	13.1	516	2	Q9M174_ARATH	Q9m174	arabidopsis	538	60	13.0	341	2	Q2L4T1_HUMAN	Q2vl55	tarsius syr
466	60.5	13.1	547	2	Q4R401_MACFA	Q4r401	macaca fasc	539	60	13.0	342	1	PAX9_MOUSE	P47242	mus musculus
467	60.5	13.1	560	2	Q5P1A5_AZOSE	Q5p1a5	azocarcus sp	540	60	13.0	342	1	PAX9_MOUSE	Q3vlk1	mus musculus
468	60.5	13.1	618	2	Q9GGM9_9POAL	Q9ggm9	carex backi	541	60	13.0	342	2	Q8BS81_MOUSE	Q8bs81	mus musculus
469	60.5	13.1	638	1	KCNC2_RAT	P22462	rattus norv	542	60	13.0	342	2	Q8BS81_MOUSE	Q8bs81	mus musculus



251	62.5	13.6	504	2	Q7S9U0_NEUCR	Q7S9U0_neurospora	324	61.5	13.3	321	2	Q44JU7_CHRSL	Q44ju7 chromohalob
252	62.5	13.6	525	2	Q9NCZ9_TRYCO	Q9ncz9 trypanosoma	325	61.5	13.3	324	2	Q3H547_9ACTO	Q3h547 nocardioide
253	62.5	13.6	525	2	Q76235_TRYCO	Q76235 trypanosoma	326	61.5	13.3	327	2	Q6MX9_DEBEA	Q6mx9 dbellovibri
254	62.5	13.6	539	2	Q9RD59_STRCO	Q9rd59 streptomyce	327	61.5	13.3	339	1	TM66_FONPY	Q5r491 pongo pygma
255	62.5	13.6	552	2	Q33287_SHEWANA	Q33287 shewanella	328	61.5	13.3	342	1	IS1A_SYNT3	Q55274 rhodocycot
256	62.5	13.6	557	2	Q7XQW8_ORYZA	Q7xqw8 oryza sativ	329	61.5	13.3	345	2	Q2RST8_RHORU	Q2rst8 rhodospirill
257	62.5	13.6	580	2	Q5T6S3_HUMAN	Q5t6s3 homo sapien	330	61.5	13.3	347	2	Q6R122_MOUSE	Q6r122 mus musculu
258	62.5	13.6	604	2	Q9VNP7_DROME	Q9vnp7 drosophila	331	61.5	13.3	381	2	Q88VV9_LACPL	Q88vv9 lactobacill
259	62.5	13.6	621	2	Q6N038_HUMAN	Q6n038 homo sapien	332	61.5	13.3	382	2	Q4Q9N5_LEIMA	Q4q9n5 leishmania
260	62.5	13.6	663	2	Q72PX8_LEPIC	Q72px8 leptospira	333	61.5	13.3	399	2	Q89MV3_BRAJA	Q89mv3 bradyrhizob
261	62.5	13.6	663	2	Q8F6A7_LEPTOSPIRA	Q8f6a7 leptospira	334	61.5	13.3	411	2	Q34009_RHOPA	Q340q9 rhodopseudo
262	62.5	13.6	670	2	Q4SQ15_TETNG	Q4sq15 tetraodon n	335	61.5	13.3	427	2	Q5WKBS_BACSK	Q5wkb5 bacillus cl
263	62.5	13.6	685	2	Q8EEJ6_SHEON	Q8eej6 shewanella	336	61.5	13.3	430	2	Q487R5_COLP3	Q487r5 colwellia p
264	62.5	13.6	700	2	Q8TG00_ASPFU	Q8tg00 aspergillus	337	61.5	13.3	433	2	Q9JS97_CHLPN	Q9js97 chlamydia p
265	62.5	13.6	760	2	Q7XNU5_ORYZA	Q7xnu5 oryza sativ	338	61.5	13.3	433	2	Q9KLT7_CHLPN	Q9klt7 chlamydia p
266	62.5	13.6	769	1	KCNC3_MOUSE	Q63959 mus musculu	339	61.5	13.3	433	2	Q9Z748_CHLPN	Q9z748 chlamydia p
267	62.5	13.6	850	2	Q6SMA9_BACLD	Q6sma9 bacillus li	340	61.5	13.3	434	2	Q736Y4_BACCL	Q736y4 bacillus ce
268	62.5	13.6	910	1	SYL_NEIMA	Q9jw39 neisseria m	341	61.5	13.3	437	2	Q8NF56_HUMAN	Q8nf56 homo sapien
269	62.5	13.6	1048	1	SILA_SALTY	Q9zhc9 salmonella	342	61.5	13.3	445	2	Q57I33_SALCH	Q57i33 salmonella
270	62.5	13.6	1048	2	Q2ZSN0_SHEPU	Q2zsn0 shewanella	343	61.5	13.3	445	2	Q5PKR4_SALPA	Q5pkr4 salmonella
271	62.5	13.6	1048	2	Q3G640_9GAMM	Q3g640 shewanella	344	61.5	13.3	445	2	Q8ZL09_SALTY	Q8ztl09 salmonella
272	62.5	13.6	1048	2	Q6MXQ0_SERMA	Q6mxq0 serratia ma	345	61.5	13.3	445	2	Q8Z2L3_SALTY	Q8z2l3 salmonella
273	62.5	13.6	1487	2	Q3NTP0_SHEFR	Q3ntp0 shewanella	346	61.5	13.3	458	2	Q6D860_ERMCT	Q6d860 erwinia car
274	62.5	13.6	1489	2	Q2JLT7_RHOPA	Q2jlt7 rhodopseudo	347	61.5	13.3	461	2	Q4FFN8_9LILI	Q4ffn8 acorus amer
275	62	13.4	150	2	Q893N4_CLOTE	Q893n4 clostridium	348	61.5	13.3	493	2	Q4CX55_TRYCR	Q4cx55 trypanosoma
276	62	13.4	179	1	DSBB_HREDU	Q7vky2 haemophilus	349	61.5	13.3	495	2	Q4SRO6_TRTNG	Q4sro6 tetraodon n
277	62	13.4	189	2	Q6X9L3_SULIS	Q6x9l3 sulfolobus	350	61.5	13.3	522	2	Q84DU5_LISIV	Q84du5 listeria iv
278	62	13.4	241	2	Q3GLJ7_9DELT	Q3glj7 pelobacter	351	61.5	13.3	523	2	Q84DU4_LISIV	Q84du4 listeria iv
279	62	13.4	269	2	Q6YVW5_ORYZA	Q6yvww5 oryza sativ	352	61.5	13.3	524	1	P60_LISIV	Q01837 listeria iv
280	62	13.4	287	2	Q3KR82_RAT	Q3kr82 rattus norv	353	61.5	13.3	545	2	Q9QEW6_9PARA	Q9qew6 measles vir
281	62	13.4	297	2	Q3BQX5_XANC5	Q3bxq5 xanthomonas	354	61.5	13.3	549	2	Q9V3U6_DROME	Q9v3u6 drosophila
282	62	13.4	308	2	Q6LXB8_CAEBR	Q6lxb8 caenorhabdi	355	61.5	13.3	566	2	Q7JL70_TREDE	Q7jlv0 treponema d
283	62	13.4	308	2	Q8BFU1_MOUSE	Q8bfu1 m 7 days ne	356	61.5	13.3	592	2	Q9PVDI_XENLA	Q9pvd1 xenopus lae
284	62	13.4	381	2	Q8UC07_AGRT5	Q8uc07 agrobacteri	357	61.5	13.3	637	2	Q36LA4_MARHY	Q36lmv1 mus musculu
285	62	13.4	393	2	Q7CWG7_AGRT5	Q7cwg7 agrobacteri	358	61.5	13.3	668	1	RN139_MOUSE	Q76mvl mus musculu
286	62	13.4	414	2	Q32383_STRGR	Q32383 streptomyce	359	61.5	13.3	701	2	Q4G0I9_HUMAN	Q4g0i9 homo sapien
287	62	13.4	416	2	Q3QHT7_9GAMM	Q3qht7 shewanella	360	61.5	13.3	805	2	Q6ZL28_BURMA	Q6zlv2 burkholderi
288	62	13.4	417	2	Q3IGF3_PSEHT	Q3igf3 pseudalter	361	61.5	13.3	807	2	Q3JTE4_BURPI	Q3jte4 burkholderi
289	62	13.4	419	2	Q7XTD2_ORYZA	Q7xtcd2 oryza sativ	362	61.5	13.3	831	2	Q60XB5_CAEBR	Q60xb5 caenorhabdi
290	62	13.4	445	2	Q96X94_SULTO	Q96x94 sulfolobus	363	61.5	13.3	854	2	Q4DIM4_TRYCR	Q4dim4 trypanosoma
291	62	13.4	445	2	Q2R394_ORYZA	Q2r394 oryza sativ	364	61.5	13.3	855	2	Q63TB1_BURPS	Q63tb1 burkholderi
292	62	13.4	470	2	Q8PBI1_XANAC	Q8pb1 xanthomonas	365	61.5	13.3	913	2	Q2KGW0_MAGGR	Q2kgw0 magnaporthe
293	62	13.4	489	2	Q6SUC0_MANSM	Q6suc0 manheimia	366	61.5	13.3	977	1	FCRL5_HUMAN	Q96rd9 homo sapien
294	62	13.4	526	2	Q2L0P8_BORAV	Q2l0p8 bordetella	367	61.5	13.3	990	2	Q32MR1_HUMAN	Q32mr1 homo sapien
295	62	13.4	558	2	Q8NIV9_HUMAN	Q8niv9 homo sapien	368	61.5	13.3	990	2	Q6Q4G3_HUMAN	Q6q4g3 homo sapien
296	62	13.4	568	2	Q2JR78_9CYAN	Q2jrt78 cyanobacter	369	61.5	13.3	998	2	Q495Q3_HUMAN	Q495q3 homo sapien
297	62	13.4	577	2	Q9V7C4_DROME	Q9v7c4 drosophila	370	61.5	13.3	1145	2	Q8GUE7_9LILI	Q8gue7 cymodocea n
298	62	13.4	581	1	FUR4_SGHO	Q10279 schizosacch	371	61.5	13.3	1322	2	Q5AL53_CANAL	Q5al53 candida alb
299	62	13.4	613	2	Q96PR0_HUMAN	Q96pr0 homo sapien	372	61.5	13.3	1499	2	Q8YK83_ANASP	Q8yk83 anabaena sp
300	62	13.4	629	2	Q86W09_HUMAN	Q86w09 homo sapien	373	61	13.2	100	2	Q6VE83_PSESY	Q6ve83 pseudomonas
301	62	13.4	638	2	Q96PR1_HUMAN	Q96pr1 homo sapien	374	61	13.2	112	2	Q2K4H0_RHET	Q2k4h0 rhizobium e
302	62	13.4	641	2	Q4LE77_HUMAN	Q4le77 homo sapien	375	61	13.2	139	2	Q87HL7_VIBPA	Q87hl7 vibrio para
303	62	13.4	777	2	Q51502_PSEAE	Q51502 pseudomonas	376	61	13.2	157	2	Q8DV17_STRMU	Q8dv17 streptococc
304	62	13.4	862	2	Q6MYC9_ASPFU	Q6myc9 aspergillus	377	61	13.2	173	2	Q7Q505_ANOGA	Q7q505 anopheles g
305	62	13.4	962	2	Q6BZ68_DEBHA	Q6bz68 debaryomyce	378	61	13.2	173	2	Q6MY22_SERMA	Q6my22 serratia ma
306	62	13.4	1035	2	Q4QGS8_LEIMA	Q4qgs8 leishmania	379	61	13.2	180	2	Q811G5_MOUSE	Q811g6 mus musculu
307	62	13.4	1057	2	Q6FTI2_CANGA	Q6fti2 candida gla	380	61	13.2	187	2	Q5HZU1_XENTR	Q5hzul xenopus tro
308	62	13.4	2325	1	SDK_CABEL	Q9n3x8 caenorhabdi	381	61	13.2	198	2	Q379H1_RHOPA	Q379h1 rhodopseudo
309	61.5	13.3	99	2	Q36L98_MARHY	Q36l98 marinobacte	382	61	13.2	200	2	Q3GEF5_9FIRM	Q3gef5 syntrophomo
310	61.5	13.3	134	2	Q6TSM0_9BACI	Q6tsm0 bacillus sp	383	61	13.2	238	2	Q5V6G2_HALMA	Q5v6g2 haloarcula
311	61.5	13.3	178	2	Q83E78_COXBV	Q83e78 coxiella bu	384	61	13.2	268	2	Q9AB59_CAUCR	Q9ab59 caulobacter
312	61.5	13.3	180	2	Q615L4_ORYSA	Q615l4 oryza sativ	385	61	13.2	272	2	Q8G9V3_ECOLI	Q8g9v3 escherichia
313	61.5	13.3	206	2	Q5JEL8_PYRKO	Q5jel8 pyrococcus	386	61	13.2	302	2	Q54880_RAT	Q54880 rattus norv
314	61.5	13.3	210	2	Q636E4_BACCC	Q636e4 bacillus ce	387	61	13.2	320	2	Q34086_COCER	Q34086 coccyzus er
315	61.5	13.3	213	2	Q8FR74_COREF	Q8fr74 coreynebacte	388	61	13.2	326	2	Q3TXR0_MOUSE	Q3txr0 mus musculu
316	61.5	13.3	216	2	Q4NJJ0_9MLCC	Q4njjo arthrobacte	389	61	13.2	326	2	Q762D5_MOUSE	Q762d5 m udp-glucu
317	61.5	13.3	216	2	Q7V8X4_PROMM	Q7v8x4 prochloroco	390	61	13.2	338	1	1GT_TREDE	P60974 treponema d
318	61.5	13.3	260	2	Q89N10_BRAJIZ	Q89n10 bradyrhizob	391	61	13.2	341	1	PAX5_SAGOE	Q95156 sagotinus oe
319	61.5	13.3	262	2	Q9NB91_AGRIP	Q9nb91 agrotis ips	392	61	13.2	355	2	Q95592_COTJA	Q95592 coturnix co
320	61.5	13.3	301	2	Q55KK5_CRYNE	Q55kk5 cryptococcu	393	61	13.2	380	2	Q7FG49_ANOGA	Q7pg49 anopheles g
321	61.5	13.3	301	2	Q5KAK4_CRYNE	Q5kak4 cryptococcu	394	61	13.2	389	2	Q7T197_CHICK	Q7t197 gallus gall
322	61.5	13.3	316	2	Q2WJL3_CLOBE	Q2wj13 clostridium	395	61	13.2	395	2	Q988F9_RHIL0	Q988f9 rhizobium l
323	61.5	13.3	330	2	Q6LFP1_PHOPR	Q6lpf1 photobacter	396	61	13.2	413	2	Q59KD6_CANAL	Q59kd6 candida alb



105	66.5	14.4	523	1	KCNA3_HUMAN	P22001	homo sapien	178	63.5	13.8	141	2	Q3FWP6_9BURK	Q3fwf6 rhodofera
106	66.5	14.4	546	2	Q5RA50_PONPY	Q5ra50 pongo pygma	179	63.5	13.8	240	2	Q49Kf1_PSEPU	Q49kf1 pseudomonas	
107	66.5	14.4	549	2	Q85W6_SHEON	Q85w6 shewanella	180	63.5	13.8	241	2	Q5UX90_HALMA	Q5ux90 haloarcula	
108	66.5	14.4	557	2	Q6P2D3_HUMAN	Q6p2d3 homo sapien	181	63.5	13.8	244	2	Q39L16_BURSA	Q39l16 burkholderi	
109	66.5	14.4	575	2	Q5VMN2_HUMAN	Q5vmn2 homo sapien	182	63.5	13.8	284	2	Q41ZES_DESMA	Q41zes desulfitoba	
110	66.5	14.4	767	2	Q2Y8H1_NITMU	Q2y8h1 nitrosospir	183	63.5	13.8	309	2	Q8Y5P7_LISMO	Q8y5p7 listeria mo	
111	66	14.3	139	2	Q5XWNO_SOLTU	Q5xwn0 solanum tub	184	63.5	13.8	309	2	Q92A05_LISIN	Q92a05 listeria in	
112	66	14.3	321	2	Q5S122_9BRAD	Q5s122 bradyrhizob	185	63.5	13.8	312	2	Q4EQD2_LISMO	Q4eqd2 listeria mo	
113	66	14.3	446	2	Q97UY7_SULSO	Q97uy7 sulfolobus	186	63.5	13.8	318	2	Q4IG61_GIBZE	Q4ig61 gibberella	
114	66	14.3	688	2	Q3I168_PSEHT	Q3i168 pseudoealter	187	63.5	13.8	327	2	Q8ZVM5_HUMAN	Q8zvm5 homo sapien	
115	65.5	14.2	161	2	Q5SN36_CRYNE	Q5sn36 cryptococcus	188	63.5	13.8	359	2	Q822F8_CHLCV	Q822f8 chlamydomophi	
116	65.5	14.2	161	2	Q5KRG5_CRYNE	Q5krg5 cryptococcus	189	63.5	13.8	372	2	Q5X4P4_LEGPA	Q5x4p4 legionella	
117	65.5	14.2	305	2	Q74DY6_GEOSL	Q74dy6 geobacter s	190	63.5	13.8	396	2	Q5UVL7_9PEZI	Q5uvl7 cercophora	
118	65.5	14.2	310	2	Q2JVO7_9CYAN	Q2jvq7 cyanobacter	191	63.5	13.8	410	2	Q4LUJ0_9BURK	Q4luj0 burkholderi	
119	65.5	14.2	333	2	Q6L3P2_SOLDE	Q6l3p2 solanum dem	192	63.5	13.8	420	2	Q6I568_ORYSA	Q6i568 oryza sativ	
120	65.5	14.2	374	2	Q2QR83_ORYSA	Q2q8r3 oryza sativ	193	63.5	13.8	452	2	Q6FVH0_CANGA	Q6fvh0 candida gla	
121	65.5	14.2	428	2	Q4OKM9_DESAC	Q4okm9 desulfoarctob	194	63.5	13.8	455	2	Q3F9X8_9BURK	Q3f9x8 burkholderi	
122	65.5	14.2	546	2	Q86V42_HUMAN	Q86v42 homo sapien	195	63.5	13.8	479	2	Q3TR92_MOUSE	Q3tr92 mus musculus	
123	65.5	14.2	546	2	Q96N39_HUMAN	Q96nj9 homo sapien	196	63.5	13.8	502	2	Q459G4_9BURK	Q459g4 burkholderi	
124	65.5	14.2	582	2	Q8N8P9_HUMAN	Q8n8p9 homo sapien	197	63.5	13.8	511	1	KCNC1_HUMAN	P48547 homo sapien	
125	65.5	14.2	1185	2	Q8SG58_SHEON	Q8sg58 shewanella	198	63.5	13.8	511	1	KCNC1_MOUSE	P15388 mus musculus	
126	65.5	14.2	1278	2	Q4SW90_TETNG	Q4sw90 tetraodon n	199	63.5	13.8	511	2	Q3KN38_HUMAN	Q3kn38 homo sapien	
127	65	14.1	100	2	Q2ITAI_RHOPA	Q2itai rhodospseudo	200	63.5	13.8	511	2	Q5BN35_RABIT	Q5bn35 oryctolagus	
128	65	14.1	134	2	Q5RI57_BRARE	Q5ri57 brachydanio	201	63.5	13.8	511	2	Q5BN36_BOVIN	Q5bn36 bos taurus	
129	65	14.1	327	2	Q9LVG3_ARATH	Q9lvq3 arabidopsis	202	63.5	13.8	511	2	Q3UHB6_MOUSE	Q3uhb6 m adult mal	
130	65	14.1	427	2	Q4U9T1_THEAN	Q4u9t1 theileria a	203	63.5	13.8	521	2	Q4V7K2_XENLA	Q4v7k2 xenopus lae	
131	65	14.1	469	2	Q9YDX1_MAGMG	Q9ydx1 magnetospir	204	63.5	13.8	550	2	Q4QEW8_9PARA	Q4qew8 measles vir	
132	65	14.1	582	2	Q5UQ22_MINIV	Q5uq22 minivir	205	63.5	13.8	564	2	Q2UHF4_ASPOR	Q2uhf4 aspergillus	
133	65	14.1	760	2	Q90638_GALL	Q90638 gallus gall	206	63.5	13.8	585	1	KCNC1_RAT	P25122 rattus norv	
134	65	14.1	832	2	Q4BS00_TETNG	Q4bs00 tetraodon n	207	63.5	13.8	585	2	Q3X5J8_CANFA	Q3x5j8 canis fami	
135	64.5	14.0	155	2	Q9R126_MOUSE	Q9r126 mus musculu	208	63.5	13.8	620	2	Q07239_MYCTU	Q07239 mycobacteri	
136	64.5	14.0	189	2	Q6C1N8_YARLI	Q6c1n8 yarrowia li	209	63.5	13.8	620	2	Q7U2A5_MYCBO	Q7u2a5 mycobacteri	
137	64.5	14.0	244	2	Q72EX5_DESVH	Q72ex5 desulfovibr	210	63.5	13.8	642	2	Q4SZN6_TETNG	Q4szn6 tetraodon n	
138	64.5	14.0	311	2	Q4HB57_9DEIO	Q4hb57 deinococcus	211	63.5	13.8	644	2	Q35Q84_9BRAD	Q35q84 bradyrhizob	
139	64.5	14.0	312	2	Q4HEH0_LISMO	Q4heh0 listeria mo	212	63.5	13.8	725	2	Q4HL36_CANLA	Q4hl36 campylobact	
140	64.5	14.0	372	2	Q71Y12_LISMP	Q71y12 listeria mo	213	63.5	13.8	747	2	Q57527_MAIZE	Q57527 zea mays (m	
141	64.5	14.0	372	2	Q5W334_LEGPL	Q5w334 legionella	214	63.5	13.8	909	2	Q4DA40_TYRCA	Q4da40 trypanosoma	
142	64.5	14.0	416	2	Q3NLN2_SHEFR	Q3nl2 shewanella	215	63	13.7	80	2	Q7NU33_CHRVO	Q7nu33 chromobacte	
143	64.5	14.0	448	2	Q3NB05_9PROT	Q3nb05 nitrosomona	216	63	13.7	125	2	Q5J333_PYRKO	Q5j333 pyrococcus	
144	64.5	14.0	452	2	Q7T165_BRARE	Q7t165 brachydanio	217	63	13.7	194	2	Q3BX62_XANC5	Q3bx62 xanthomonas	
145	64.5	14.0	455	2	Q87XZ5_PYRPU	Q87x5 pyrococcus	218	63	13.7	201	2	Q31NJ4_SYNP7	Q31nj4 synechococc	
146	64.5	14.0	465	2	Q86080_RHOSH	Q86080 rhodobacter	219	63	13.7	201	2	Q5N5M0_SYNP6	Q5n5m0 synechococc	
147	64.5	14.0	465	2	Q3IXA5_RHOSA	Q3ixa5 rhodobacter	220	63	13.7	339	2	Q3G277_9ACTO	Q3g277 nocardioid	
148	64.5	14.0	550	2	Q9QEW7_9PARA	Q9qew7 measles vir	221	63	13.7	378	2	Q7QFG1_ANOGA	Q7qfg1 anopheles g	
149	64.5	14.0	550	2	Q9QEW7_9PARA	Q9qew7 measles vir	222	63	13.7	417	2	Q375X8_RHOPA	Q375x8 rhodospseudo	
150	64.5	14.0	633	2	Q4SHG0_TETNG	Q4shg0 tetraodon n	223	63	13.7	465	2	Q4PDK1_USTMA	Q4pdk1 ustilago ma	
151	64.5	14.0	677	2	Q5GUQ5_XANOR	Q5guq5 xanthomonas	224	63	13.7	467	2	Q4I5E1_GIBZE	Q4i5e1 gibberella	
152	64.5	14.0	725	2	Q8SY05_DROME	Q8sy05 drosophila	225	63	13.7	468	2	Q9ZVA7_ARATH	Q9zva7 arabidopsis	
153	64.5	14.0	871	2	Q5A4X3_CANAL	Q5a4x3 candida alb	226	63	13.7	496	2	Q7NB28_MYCGA	Q7nb28 mycoplasma	
154	64.5	14.0	920	2	Q6XR97_9BACT	Q6xr97 uncultured	227	63	13.7	622	2	Q59QV3_CANAL	Q59qv3 candida alb	
155	64.5	14.0	1750	2	Q4WRY3_9BACT	Q4wry3 aspergillus	228	63	13.7	655	2	Q8KW19_STRMU	Q8kw19 streptococc	
156	64.5	14.0	2281	2	Q3F3Z0_9BURK	Q3f3z0 burkholderi	229	63	13.7	655	2	Q8DUN3_CANAL	Q8dun3 streptococc	
157	64	13.9	186	2	Q4RHT5_TETNG	Q4rht5 tetraodon n	230	63	13.7	750	2	Q59R09_CANAL	Q59r09 candida alb	
158	64	13.9	244	2	Q4BB11_BURVI	Q4bb11 burkholderi	231	63	13.7	808	2	Q6DD69_XENLA	Q6dd69 xenopus lae	
159	64	13.9	250	2	Q7WU64_9THEM	Q7wu64 thermotoga	232	63	13.7	825	2	Q933G5_9GAMA	Q933g5 callitrichi	
160	64	13.9	303	2	Q4KGC4_PSEFS	Q4kgc4 pseudomonas	233	63	13.7	917	2	Q8D4M3_VIBVU	Q8d4m3 vibrio vuln	
161	64	13.9	315	2	Q9LSS8_ARATH	Q9lss8 arabidopsis	234	63	13.7	917	2	Q5E8X2_VIBF1	Q5e8x2 vibrio fisc	
162	64	13.9	340	2	Q72W35_LEPIC	Q72w35 leptospira	235	63	13.7	923	2	Q9N389_CABEL	Q9n389 caenothabdi	
163	64	13.9	383	2	Q6N5J0_RHOPA	Q6n5j0 rhodospseudo	236	63	13.7	1022	2	Q27779_SCHMA	Q27779 schistosoma	
164	64	13.9	436	2	Q86VR7_HUMAN	Q86vr7 homo sapien	237	63	13.7	1411	2	Q5AS38_EMENI	Q5as38 aspergillus	
165	64	13.9	524	2	Q475P1_RALEJ	Q475p1 ralstonia e	238	62.5	13.6	146	2	Q81GV1_BACCR	Q81gv1 bacillus ce	
166	64	13.9	525	1	KCNA3_RAT	P15384 rattus norv	239	62.5	13.6	148	2	Q3EZR6_BACTI	Q3ezr6 bacillus th	
167	64	13.9	582	2	Q6K620_ORYSA	Q6k620 oryza sativ	240	62.5	13.6	160	2	Q3EPEO_SCHJA	Q3ep60 schistosoma	
168	64	13.9	667	2	Q9B5M1_TRISP	Q9b5m1 trichinella	241	62.5	13.6	163	2	Q73CB6_BACCI	Q73cb6 bacillus ce	
169	64	13.9	678	2	Q8R9G1_THETN	Q8r9g1 thermoanaer	242	62.5	13.6	174	2	Q3Q4C2_9GAMM	Q3q4c2 shewanella	
170	64	13.9	727	2	Q6FIK3_CANGA	Q6fik3 candida gla	243	62.5	13.6	207	2	Q8TBL6_HUMAN	Q8tbl6 homo sapien	
171	64	13.9	774	2	Q3JTQ0_BURP1	Q3jtg0 burkholderi	244	62.5	13.6	286	2	Q9BSB3_HUMAN	Q9bsb3 homo sapien	
172	64	13.9	804	2	Q7SGV0_ORYSA	Q7sgv0 oryza sativ	245	62.5	13.6	299	1	COMQ_BACSU	P33690 bacillus su	
173	64	13.9	915	2	Q7MG71_VIBVY	Q7mg71 vibrio vuln	246	62.5	13.6	339	1	TMM66_HUMAN	Q96by9 homo sapien	
174	64	13.9	1046	2	Q82WK5_NITEU	Q82wk5 nitrosomona	247	62.5	13.6	372	2	Q5ZUY1_LEGPH	Q5zuy1 legionella	
175	64	13.9	1155	2	Q2NT22_SODGL	Q2nt22 sodalite glo	248	62.5	13.6	434	2	Q6HHZ7_BACCH	Q6hhz7 bacillus th	
176	63.5	13.8	63	2	Q3CK79_THETN	Q3ck79 thermoanaer	249	62.5	13.6	434	2	Q81PR7_BACAN	Q81pr7 bacillus an	
177	63.5	13.8	83	2	Q41HR9_9BACI	Q41hr9 exigibacte	250	62.5	13.6	492	2	Q750E3_ASHGO	Q750e3 ashbya goss	

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OM protein - protein search, using sw model

Run on: November 21, 2006, 19:46:39 ; Search time 301 Seconds  
(without alignments)  
273.510 Million cell updates/sec

Title: US-10-063-557-50  
Perfect score: 461  
Sequence: 1 MERVYIALLLAGLTALLEAN.....HSPVPEKAIPITPGSATTC 89

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database : Uniprot 7.2.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	461	100.0	89	2	Q6UWZ1_HUMAN
2	452	98.0	89	2	Q7Z4M5_HUMAN
3	450	97.6	89	1	FXYP4_HUMAN
4	276.5	60.0	88	1	FXYP4_MOUSE
5	256.5	55.6	87	1	FXYP4_RAT
6	241.5	52.4	88	1	FXYP3_MOUSE
7	241.5	52.4	88	2	Q3TDM3_MOUSE
8	234.5	50.9	88	1	FXYP3_RAT
9	230.5	50.0	88	1	FXYP3_HUMAN
10	214.5	46.5	87	1	FXYP3_MOUSE
11	214.5	46.5	87	2	Q6IB59_HUMAN
12	203	44.0	70	2	Q80UV3_MOUSE
13	131.5	28.5	92	2	Q3SZX0_BOVIN
14	129	28.0	92	1	PLM_HUMAN
15	127.5	27.7	88	2	Q4RFG2_TETNG
16	126.5	27.4	92	1	PLM_CANFA
17	124.5	27.0	94	1	FXYP6_RAT
18	123.5	26.8	94	1	FXYP6_MOUSE
19	119	25.8	100	2	Q5MBE9_XENTR
20	116.5	25.3	95	2	Q3MHZ5_BOVIN
21	116	25.2	94	2	Q70Q12_SQUAC
22	115.5	25.1	92	1	PLM_MOUSE
23	115	24.9	95	1	FXYP6_PONPY
24	113.5	24.6	95	2	Q6DJF4_XENLA
25	113	24.5	92	1	PLM_RAT
26	112.5	24.4	95	1	FXYP6_HUMAN
27	112.5	24.4	95	1	FXYP6_MACFA
28	110	23.9	95	2	Q5ZM59_CHICK
29	107.5	23.3	87	2	Q4RHT7_TETNG
30	103.5	22.5	94	2	Q6JDJ6_XENLA
31	96.5	20.9	58	1	ATNG_BOVIN

32	96	20.8	99	2	Q7SZ52_BRARE	Q7sz52 brachydanio
33	95.5	20.7	53	1	ATNG_SHEEP	Q04680 ovis aries
34	95.5	20.7	65	2	Q58K79_PIG	Q08k79 sus scrofa
35	94	20.4	178	1	FXYS_HUMAN	Q96db9 homo sapien
36	93	20.2	178	2	Q3TDM1_MOUSE	Q3tdw1 m nod-deriv
37	92	20.0	178	1	FXYS_RAT	P59647 rattus norv
38	92	20.0	178	2	Q6P9W0_RAT	Q6p9w0 rattus norv
39	89.5	19.4	78	2	Q3ZBJ3_BOVIN	Q3zbj3 bos taurus
40	89	19.3	80	1	FXYP7_HUMAN	P59549 homo sapien
41	85	18.4	80	1	FXYP7_MOUSE	P59648 mus musculu
42	84	18.2	178	2	Q8IWS1_HUMAN	Q8iws1 homo sapien
43	83	18.0	66	1	ATNG_HUMAN	P54710 homo sapien
44	83	18.0	80	1	FXYP7_RAT	P59649 rattus norv
45	83	18.0	94	1	FXYP8_HUMAN	P59550 homo sapien
46	82.5	17.9	66	1	ATNG_RAT	Q04679 rattus norv
47	79.5	17.2	142	2	Q6P8R9_MOUSE	Q6p8r9 mus musculu
48	78	16.9	70	1	ATNG_MOUSE	Q04646 mus musculu
49	78	16.9	70	2	Q6ITT2_MOUSE	Q6itt2 mus musculu
50	77.5	16.8	711	2	Q4NGJ7_9MIC	Q4ngj7 arthrobacte
51	76	16.5	289	2	Q4WU10_ASPFU	Q4wu10 aspergillus
52	75.5	16.4	524	2	Q5LOV1_SILPO	Q5lqv1 silicibacte
53	74	16.1	188	2	Q5LM65_SILPO	Q5lw65 silicibacte
54	74	16.1	208	2	Q4R6E0_MACFA	Q4r6e0 macaca fasc
55	73.5	15.9	64	2	Q6ITT1_MOUSE	Q6itt1 mus musculu
56	73.5	15.9	82	2	Q6ITTO_MOUSE	Q6itto mus musculu
57	73.5	15.9	196	2	Q9CZE7_CABEL	Q9cze7 caenorhabdi
58	73.5	15.9	330	2	Q84EY9_ENTCL	Q84ey9 enterobacte
59	73	15.8	201	2	Q7QJ63_ANOGA	Q7qj63 anopheles g
60	73	15.8	455	2	Q4IPU0_GIBZE	Q4ipu0 gibberella
61	73	15.8	1132	2	Q83861_9REOV	Q83861 nilaparvata
62	72	15.6	160	1	PTD_SYNY3	P27589 synechocyst
63	71	15.4	61	1	ATNG_XENLA	Q13001 xenopus lae
64	71	15.4	529	2	Q34355_BACSU	Q34355 bacillus su
65	71	15.4	577	2	Q4A723_MYCDS	Q4a723 mycoplasma
66	70.5	15.3	251	2	Q54FJ8_DICDI	Q54fj8 dictyosteli
67	70.5	15.3	334	2	Q6D644_ERWCT	Q6d644 erwinia car
68	70	15.2	184	1	FXYP5_MOUSE	P97808 mus musculu
69	70	15.2	216	2	Q5ZFS6_PLAMJ	Q5zfs6 plantago ma
70	69.5	15.1	236	2	Q6GME4_XENLA	Q6gme4 xenopus lae
71	69.5	15.1	268	2	Q4PSL8_PSYAR	Q4psl8 psychrobact
72	69.5	15.1	458	2	Q5KUP7_GEOKA	Q5kup7 geobacillus
73	69	15.0	150	2	Q668G1_YERPS	Q668g1 versinia ps
74	69	15.0	150	2	Q8ZCD4_YERPE	Q8zcd4 versinia pe
75	69	15.0	146	2	Q8DOY1_YERPE	Q8doy1 versinia pe
76	68.5	14.9	157	2	Q36ZXA_RIOPA	Q36zxa rhodopseudo
77	68.5	14.9	339	2	Q9LUX8_ARATH	Q9lux8 arabidopsis
78	68.5	14.9	340	2	Q94E19_ARATH	Q94e19 arabidopsis
79	68.5	14.9	344	2	Q3X714_METFL	Q3x714 methylobacti
80	68.5	14.9	456	2	Q9CL30_PASMU	Q9cl30 pasteurella
81	68.5	14.9	485	2	Q58EK5_BRARE	Q58ek5 brachydanio
82	68.5	14.9	499	2	Q5VHU5_CIOIN	Q5vhu5 ciona intes
83	68.5	14.9	531	2	Q5VHU5_CIOIN	Q5vhu5 ciona intes
84	68	14.8	173	2	Q4HKR3_9PERC	Q4hkr3 arcos sp. k
85	68	14.8	417	2	Q8QD23_LEIMA	Q8qd23 leishmania
86	68	14.8	978	2	Q69SP5_ORYSA	Q69sp5 oryza sativ
87	67.5	14.6	135	1	YCF56_MARPO	Q32616 marchantia
88	67.5	14.6	216	2	Q3EKS3_BACTI	Q3eks3 bacillus th
89	67.5	14.6	227	2	Q37UP8_SPHAR	Q37up8 novosphingo
90	67.5	14.6	337	2	Q6L3V4_SOLDE	Q6l3v4 solanum dem
91	67.5	14.6	387	2	Q6YYV7_ORYSA	Q6yyv7 oryza sativ
92	67.5	14.6	664	1	RN139_HUMAN	Q8wu17 homo sapien
93	67.5	14.6	664	2	Q5RBT7_PONPY	Q5rbt7 pongo pygma
94	67	14.5	227	2	Q2W8Y8_MAGSA	Q2w8y8 magnetospir
95	67	14.5	364	2	Q5ZFS7_PLAMJ	Q5zfs7 plantago ma
96	67	14.5	390	1	AROC_SULTO	Q96y94 sulfobobir
97	67	14.5	715	2	Q72E54_DESVH	Q72e54 desulfovibr
98	66.5	14.4	174	2	Q3PM00_NITHA	Q3pm00 nitrobacter
99	66.5	14.4	241	2	Q9KJ13_STPCO	Q9kj13 streptomyce
100	66.5	14.4	263	2	Q4B4Z0_9BURK	Q4b4z0 polaromonas
101	66.5	14.4	329	2	Q6OD39_SOLTU	Q6od39 solanum tub
102	66.5	14.4	359	1	AROC_CHLNP	Q9z6m2 chlamydia p
103	66.5	14.4	408	2	Q3PM48_NITHA	Q3pm48 nitrobacter
104	66.5	14.4	516	2	Q28656_RABIT	Q28656 oryctolagus

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deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;  
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrrell,  
Nature 413, 523-527, 2001  
A:Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.  
A:Reference number: AB0001; MUID:21470413; PMID:11586360  
A:Accession: AH0371  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-150 <RUR>  
A:Cross-references: UNIPROT:Q8ZCD4; UNIPARC:UPI00000CD9C4; GB:AL590842; PIDN:CAC92299.1;  
C:Genetics:  
A:Gene: YPO3057  
C:Superfamily: hypothetical protein ytwi

Query Match 15.0%; Score 69; DB 2; Length 150;  
Best Local Similarity 30.2%; Pred. No. 2.7;  
Matches 26; Conservative 14; Mismatches 32; Indels 14; Gaps 4;

QY 4 VTLALLAGLTALEANDPFANKDPFYDWNKQLSLGICGGLLAIAIGI-AAVLSGKCK 62  
DB 26 VTLAILLAIIRITPLNS-----FFPW--VEKYGLTIGVLITIGVMAPIASG--K 72

QY 63 YKSSQKQHSVPPEKAIPITPGSATT 88  
DB 73 ISASEVLHSHFVQKSLAIVVGAVS 98

RESULT 12  
A05009  
hypothetical protein 135 - liverwort (Marchantia polymorpha) chloroplast  
C:Species: chloroplast Marchantia polymorpha  
C:Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 09-Jul-2004  
C:Accession: S01571; A05009  
R:Umesono, K.; Inokuchi, H.; Shiki, Y.; Takeuchi, M.; Chang, Z.; Fukuzawa, H.; Kohchi, T  
J. Mol. Biol. 203, 299-331, 1988  
A:Title: Structure and organization of Marchantia polymorpha chloroplast genome. II. Gen  
A:Reference number: S01567; MUID:89068686; PMID:2974085  
A:Accession: S01571  
A:Molecule type: DNA  
A:Residues: 1-135 <UME>  
A:Cross-references: UNIPROT:Q32616; UNIPARC:UPI000013A518; EMBL:X04465; NID:g11640; PIDN  
R:Ohvama, K.; Fukuzawa, H.; Kohchi, T.; Shirai, H.; Sano, T.; Sano, S.; Umesono, K.; Shi  
Nature 322, 572-574, 1986  
A:Title: Chloroplast gene organization deduced from complete sequence of liverwort March  
A:Reference number: A38014  
A:Contents: annotation; gene organization, sites, features  
C:Genetics:  
A:Gene: chloroplast  
A:Introns: 36/1  
C:Superfamily: hypothetical protein 135  
C:Keywords: chloroplast

Query Match 14.6%; Score 67.5; DB 2; Length 135;  
Best Local Similarity 32.6%; Pred. No. 3.6;  
Matches 15; Conservative 11; Mismatches 13; Indels 7; Gaps 2;

QY 9 LLLAG--LTALEANDPFANKDPFYDWNKQLSLGICGGLLAIAIG 52  
DB 16 LIIIGLFLYALKREPVSRYDFFP-----SCIGLLCGGILFFQG 56

RESULT 13  
B86620  
chorismate synthase [imported] - Chlamydomophila pneumoniae (strain J138)  
C:Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C:Accession: B86620  
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is  
Nucleic Acids Res. 28, 2311-2314, 2000  
A:Title: Comparison of whole genome sequences of Chlamydia pneumoniae J138.  
A:Reference number: A86491; MUID:20330349; PMID:10871362  
A:Accession: B86620  
A:Status: preliminary

A:Molecule type: DNA  
A:Residues: 1-359 <STO>  
A:Cross-references: UNIPROT:Q9ZGM2; UNIPARC:UPI0000125F94; GB:BA000008; NID:g8979410; PII  
A:Experimental source: strain J138  
C:Genetics:  
A:Gene: aroC  
C:Superfamily: chorismate synthase

Query Match 14.4%; Score 66.5; DB 2; Length 359;  
Best Local Similarity 23.6%; Pred. No. 13;  
Matches 25; Conservative 14; Mismatches 36; Indels 31; Gaps 4;

QY 7 ALLLAGLTALEANDPFANKD-----DPFYDWNKQLSLGICGGLLAIAIGIAAVLSG 59  
DB 234 ALMSIPAAKGFEGKGFASAQMRGSQYTDPPFMEGENITLKSNNCGGTIGGTTIGVPIRG 293

QY 60 KCKYK--SSQK-----QHSP-VPEKAIPLI 81  
DB 294 RIAPKPTSSIKRPCATVTTKKETTYPQTGRHDPVCAIRAVPVV 339

RESULT 14  
A72004  
chorismate synthase CP0815 [imported] - Chlamydomophila pneumoniae (strains CWL029 and AR3;  
C:Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae  
C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
C:Accession: A72004; D81536  
R:Kaiman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;  
Nature Genet. 21, 385-389, 1999  
A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.  
A:Reference number: A72000; MUID:99206606; PMID:10192388  
A:Accession: A72004  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-359 <AR>  
A:Cross-references: UNIPROT:Q9ZGM2; UNIPARC:UPI0000125F94; GB:AE001684; GB:AE001363; NID:  
A:Experimental source: strain CWL029  
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, I  
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,  
Nucleic Acids Res. 28, 1397-1406, 2000  
A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.  
A:Reference number: A81500; MUID:2010255; PMID:10684935  
A:Accession: D81536  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-359 <REA>  
A:Cross-references: UNIPARC:UPI0000125F94; GB:AE002240; GB:AE002161; NID:g7189720; PIDN:  
A:Experimental source: strain AR39, HL cells  
C:Genetics:  
A:Gene: aroC; CP0815  
C:Superfamily: chorismate synthase

Query Match 14.4%; Score 66.5; DB 2; Length 359;  
Best Local Similarity 23.6%; Pred. No. 13;  
Matches 25; Conservative 14; Mismatches 36; Indels 31; Gaps 4;

QY 7 ALLLAGLTALEANDPFANKD-----DPFYDWNKQLSLGICGGLLAIAIGIAAVLSG 59  
DB 234 ALMSIPAAKGFEGKGFASAQMRGSQYTDPPFMEGENITLKSNNCGGTIGGTTIGVPIRG 293

QY 60 KCKYK--SSQK-----QHSP-VPEKAIPLI 81  
DB 294 RIAPKPTSSIKRPCATVTTKKETTYPQTGRHDPVCAIRAVPVV 339

RESULT 15  
A38101  
potassium channel KCNA3 - human  
N:Alternate names: potassium channel HUK3; potassium channel PCN3; shaker-related potassi  
C:Species: Homo sapiens (man)  
C:Date: 07-Apr-1994 #sequence\_revision 07-Apr-1994 #text\_change 09-Jul-2004  
C:Accession: A38101; B38556; I52990  
R:Attali, B.; Romey, G.; Honore, E.; Schmid-Alliana, A.; Mattei, M.G.; Lesage, F.; Ricard

A;Residues: 1-160 <KAN>  
A/Cross-references: UNIPARC:UPI0000131690; EMBL:D64000; GB:AB001339; NID:g1001484; PIDN:  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996  
C;Genetics:  
A;Gene: petD  
C/Superfamily: cytochrome b6-f complex, subunit 4 (plastoquinol-plastocyanin reductase, 1  
F;2-144/Domain: plastoquinol-plastocyanin reductase 17K protein homology <17K>

Query Match 15.6%; Score 72; DB 1; Length 160;  
Best Local Similarity 37.7%; Pred. No. 1.4;  
Matches 23; Conservative

Qy 7 ALLLAGLTAL-----EANDPFANKDD--PFYDWKNQLSGLICGGLLATAGIAVLVS 58  
|||:||| : ||| : | : : ||| :  
Db 47 ALGLTAGLAILDPAMIGBPADFPFTPLBILPEWYLPTFQILRLPFLKLGAGMAAIPL 106

Qy 59 G 59  
|  
Db 107 G 107

RESULT 10  
F69989  
conserved hypothetical protein ytcJ - Bacillus subtilis  
C/Species: Bacillus subtilis  
C/Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
C/Accession: F69989  
R/Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter  
C.; Bron, S.; Broutillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch  
A.; Ehrlich, S.D.; Emmeron, P.T.; Enright, K.D.; Errington, J.; Fabret, C.; Ferrari, E.  
Nature 390, 249-256, 1997  
A/Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallert  
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hulio, M.F.;  
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,  
A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue  
Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetel  
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon  
A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sakiguchi, J.; Sekowska, A.; Seror,  
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,  
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yanane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.  
A.; Authors: Yoshikawa, H.F.; Zumbastein, E.; Yoshikawa, H.; Danchin, A. Bacillus subtilis.  
A;/Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
A;/Reference number: A69580; MUID:98044033; PMID:9384377  
A/Accession: F69989  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-529 <KUN>  
A/Cross-references: UNIPROT:I034355; UNIPARC:UPI0000060854; GB:Z99119; GB:AL009126; NID:G9  
A/Experimental source: strain 168  
C/Genetics:  
A;Gene: ytcJ

Query Match 15.4%; Score 71; DB 2; Length 529;  
Best Local Similarity 30.4%; Pred. No. 6.2;  
Matches 31; Conservative

Qy 16 ALEANDPFANKDDPPYD-----WKNLQSLGICGG-----LLAIAAG 52  
||| : | : | : ||| :  
Db 391 ALDLQPHVASFDPFWIIDLGHDKRWKTFAFKTLISKGLICAGGSAPTEVPDLGIQ- 439

Qy 53 IAAVLGSKCKVKSSOKQHSP-----VP-EKAIFLITPGSA 86  
||| : | : | : ||| :  
Db 440 -SAVLR-----KSSHEQGQPSYNESECLPVYEAKLYTGESA 475

RESULT 11  
AH0371  
probable membrane protein YPO3057 [imported] - Yersinia pestis (strain CO92)  
C/Species: Yersinia pestis  
C/Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Jul-2004  
C/Accession: AH0371  
R./Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.







1271	49	10.6	618	2	F84409	arsenite transport	1344	48.5	10.5	269	2	G87134	enoyl-[ACP] reduct
1272	49	10.6	629	2	S29685	retroviral recepto	1345	48.5	10.5	273	2	J50172	chlorophyll a/b-bi
1273	49	10.6	642	2	S29685	threonine-CrNA lig	1346	48.5	10.5	276	2	D41044	octopine-binding p
1274	49	10.6	660	2	C84944	xanthophyll epoxid	1347	48.5	10.5	277	2	D64666	glutamine ABC tran
1275	49	10.6	672	2	A65024	Hydrogenase-4 comp	1348	48.5	10.5	278	2	G71849	amino acid ABC tra
1276	49	10.6	672	2	D85891	Hydrogenase-4 memb	1349	48.5	10.5	278	2	AB2254	hypothetical prote
1277	49	10.6	672	2	H91046	hydrogenase 4 memb	1350	48.5	10.5	283	2	B86331	F6f9.15 protein -
1278	49	10.6	680	2	T29871	hypothetical prote	1351	48.5	10.5	283	2	D71130	probable oligopept
1279	49	10.6	719	2	S63392	probable membrane	1352	48.5	10.5	290	2	F71167	hypothetical prote
1280	49	10.6	740	2	T03847	Fas-binding protei	1353	48.5	10.5	301	2	F81444	probable integrat
1281	49	10.6	748	1	I50699	cytosolic phosphol	1354	48.5	10.5	302	2	A75432	3-hydroxybutyryl-C
1282	49	10.6	784	2	JH0101	apolipoprotein B-1	1355	48.5	10.5	312	2	I40201	mgE protein - Bac
1283	49	10.6	796	2	E87636	TonB-dependent rec	1356	48.5	10.5	318	2	B91177	probable hemin per
1284	49	10.6	799	2	T48690	hypothetical prote	1357	48.5	10.5	330	2	C86023	hypothetical prote
1285	49	10.6	812	2	AG3138	fimbrial usher pro	1358	48.5	10.5	332	2	AC0260	hypothetical phage
1286	49	10.6	812	2	D98149	hypothetical prote	1359	48.5	10.5	334	2	C81794	hypothetical prote
1287	49	10.6	816	2	T21713	hypothetical prote	1360	48.5	10.5	340	2	E83126	ferric enterobacti
1288	49	10.6	839	2	S35319	nucleoporin-intera	1361	48.5	10.5	342	2	E71359	hypothetical prote
1289	49	10.6	862	2	S64821	probable membrane	1362	48.5	10.5	355	2	T47527	hypothetical prote
1290	49	10.6	952	2	E84534	hypothetical prote	1363	48.5	10.5	365	2	F87552	dprA protein [limp
1291	49	10.6	969	2	F71418	hypothetical prote	1364	48.5	10.5	370	2	AS0289	conserved hypothet
1292	49	10.6	975	2	T22788	hypothetical prote	1365	48.5	10.5	372	2	C39371	Ig V-region-like B
1293	49	10.6	976	2	S40697	processing endopro	1366	48.5	10.5	382	2	A10040	probable methanol
1294	49	10.6	1041	2	B81281	probable SEC 3.2.	1367	48.5	10.5	387	2	H88012	protein K10B4.2 (i
1295	49	10.6	1054	2	T30933	chitinase (EC 3.2.	1368	48.5	10.5	388	2	T33908	hypothetical prote
1296	49	10.6	1073	1	OYHUHX	heat-stable entero	1369	48.5	10.5	394	2	E81940	two-component resp
1297	49	10.6	1086	2	T40354	hypothetical prote	1370	48.5	10.5	398	2	F75417	L-sorbose dehydr
1298	49	10.6	1190	2	T00842	probable histidine	1371	48.5	10.5	400	2	AG1208	cell-division prot
1299	49	10.6	1207	2	T52459	sensory transducti	1372	48.5	10.5	405	2	AB1565	cell-division prot
1300	49	10.6	1230	2	S47466	cellulose 1,4-beta	1373	48.5	10.5	401	2	B72329	hypothetical prote
1301	49	10.6	1265	2	T51314	probable CO-induce	1374	48.5	10.5	406	2	T31778	hypothetical prote
1302	49	10.6	1396	2	S36851	L-shaped tail fibe	1375	48.5	10.5	409	2	B85735	probable membrane
1303	49	10.6	1430	2	AF0351	probable autotrans	1376	48.5	10.5	410	2	C86835	hypothetical prote
1304	49	10.6	1530	2	E82085	glutamate synthase	1377	48.5	10.5	416	2	T02194	probable peccinase
1305	49	10.6	1648	2	F84833	probable SNF2/SWI2	1378	48.5	10.5	421	2	E90883	hypothetical prote
1306	49	10.6	2172	2	T20145	cellulose 7.5 k	1379	48.5	10.5	424	2	T31978	hypothetical prote
1307	49	10.6	3164	1	WMBEH6	UL36 protein - hum	1380	48.5	10.5	425	2	T25873	hypothetical prote
1308	48.5	10.5	73	2	D91146	hypothetical prote	1381	48.5	10.5	426	2	B75434	UDP-N-acetylglucos
1309	48.5	10.5	73	2	H85991	hypothetical prote	1382	48.5	10.5	426	2	T45767	hypothetical prote
1310	48.5	10.5	73	2	E65119	hypothetical 7.5 k	1383	48.5	10.5	431	2	H70731	hypothetical prote
1311	48.5	10.5	75	2	T45361	hypothetical prote	1384	48.5	10.5	436	2	I39973	probable esterase
1312	48.5	10.5	115	1	SPRBG	substance P gamma	1385	48.5	10.5	436	2	H70731	alkaline serine pr
1313	48.5	10.5	116	2	AD2124	hypothetical prote	1386	48.5	10.5	441	2	H98009	hypothetical prote
1314	48.5	10.5	139	2	G71033	hypothetical prote	1387	48.5	10.5	443	2	H70430	K+ transport prote
1315	48.5	10.5	146	1	A47481	interleukin-13 pre	1388	48.5	10.5	461	2	C98120	glycerol-3-phospha
1316	48.5	10.5	165	2	A31635	neural cell adhesi	1389	48.5	10.5	463	2	E81141	xanthine/uracil pe
1317	48.5	10.5	171	2	JE0153	mitochondrial inne	1390	48.5	10.5	467	2	T32292	hypothetical prote
1318	48.5	10.5	180	2	I40562	hypothetical 20.1k	1391	48.5	10.5	470	1	P2WL39	L2 protein - human
1319	48.5	10.5	183	2	B81237	hypothetical prote	1392	48.5	10.5	473	2	T17260	hypothetical prote
1320	48.5	10.5	183	2	G82008	probable integral	1393	48.5	10.5	475	2	T08753	hypothetical prote
1321	48.5	10.5	193	2	C97891	hypothetical prote	1394	48.5	10.5	478	2	D84895	probable membrane
1322	48.5	10.5	198	2	S75989	endopeptidase Clp	1395	48.5	10.5	500	2	AD1047	probable amino aci
1323	48.5	10.5	199	2	T38524	ATP synthase subun	1396	48.5	10.5	509	2	A96563	probable protein k
1324	48.5	10.5	199	2	A69859	hypothetical prote	1397	48.5	10.5	510	2	B72007	conserved hypothet
1325	48.5	10.5	208	2	C69697	protein K02B9.4 (i	1398	48.5	10.5	511	2	H90439	hypothetical prote
1326	48.5	10.5	211	2	C59091	hypothetical prote	1399	48.5	10.5	518	2	T05196	hypothetical prote
1327	48.5	10.5	217	2	A98196	hypothetical prote	1400	48.5	10.5	528	2	E81186	L-lactate permease
1328	48.5	10.5	221	2	D64907	membrane protein y	1401	48.5	10.5	537	2	A75123	proline permease (
1329	48.5	10.5	225	2	F81977	hypothetical prote	1402	48.5	10.5	546	1	VGNZRK	cell fusion glycop
1330	48.5	10.5	225	2	A86043	probable transposa	1403	48.5	10.5	546	2	S47305	gene F protein - r
1331	48.5	10.5	226	2	T23233	hypothetical prote	1404	48.5	10.5	553	2	C84920	hypothetical prote
1332	48.5	10.5	235	2	AC2809	conserved hypothet	1405	48.5	10.5	553	2	T06499	hypothetical prote
1333	48.5	10.5	235	2	H97587	hypothetical 25.1k	1406	48.5	10.5	556	2	S68408	hypothetical prote
1334	48.5	10.5	241	2	D84138	hypothetical prote	1407	48.5	10.5	559	2	C75286	methyl-accepting c
1335	48.5	10.5	243	2	B96010	conserved hypothet	1408	48.5	10.5	578	2	B82204	probable acyl-coas
1336	48.5	10.5	245	2	E97425	flagellar biosynth	1409	48.5	10.5	583	2	A70723	probable acyl-coas
1337	48.5	10.5	245	2	AE2643	flagellar biosynth	1410	48.5	10.5	584	1	VCWSIA	env polyprotein pr
1338	48.5	10.5	256	2	D86544	NADH (ubiquinone)	1411	48.5	10.5	590	2	C86465	probable inositol
1339	48.5	10.5	256	2	H72078	probable sodium-tr	1412	48.5	10.5	598	2	A69609	carbon starvation
1340	48.5	10.5	257	2	A12741	conserved hypothet	1413	48.5	10.5	601	2	G96558	probable protein k
1341	48.5	10.5	257	2	H97522	hypothetical prote	1414	48.5	10.5	605	2	T15291	sphingomyelin phos
1342	48.5	10.5	257	2	G87509	hypothetical prote	1415	48.5	10.5	608	2	C95255	hypothetical prote
1343	48.5	10.5	258	2	H70487	cytochrome-c oxida	1416	48.5	10.5	610	2	A11110	two-component sens

1125	49.5	10.7	1461	2	A85547	hypothetical prote	1198	49	10.6	355	2	S41686	geranylgeranyltran
1126	49.5	10.7	1492	2	A39322	cystic fibrosis tr	1199	49	10.6	366	2	A64950	membrane-bound pen
1127	49.5	10.7	2150	2	T08165	RNA1 polypeptoin -	1200	49	10.6	366	2	C95800	probable cytochrom
1128	49.5	10.7	2222	1	A36028	DNA-directed DNA p	1201	49	10.6	366	2	G30951	probable cytochrom
1129	49.5	10.7	2403	2	T30875	PRP8 protein homol	1202	49	10.6	367	2	G96770	hypothetical prote
1130	49.5	10.7	2500	1	WMHUE2	HIV-EP2 enhancer-b	1203	49	10.6	370	2	AB0602	probable membrane
1131	49.5	10.7	3655	2	T38084	TRAP-like protein	1204	49	10.6	378	2	F64446	chorismate synthas
1132	49	10.6	98	2	T17363	NADH2 dehydrogenas	1205	49	10.6	379	2	E69332	heterodisulfide re
1133	49	10.6	98	2	T17177	NADH2 dehydrogenas	1206	49	10.6	380	2	T11033	ubiquinol-cytochro
1134	49	10.6	99	2	D75182	lsu ribosomal prot	1207	49	10.6	382	2	A82056	hypothetical prote
1135	49	10.6	129	2	T28983	hypothetical prote	1208	49	10.6	385	2	A86227	hypothetical prote
1136	49	10.6	135	2	F86053	hypothetical prote	1209	49	10.6	391	2	T39673	probable mannosylt
1137	49	10.6	135	2	D91207	hypothetical prote	1210	49	10.6	396	2	T35024	probable glutathio
1138	49	10.6	135	2	A65171	ol35 protein - Esc	1211	49	10.6	400	2	C83511	flagellar protein
1139	49	10.6	137	1	JC4877	phospholipase A2 h	1212	49	10.6	404	2	B86962	probable secreted
1140	49	10.6	140	2	S74898	hypothetical prote	1213	49	10.6	408	2	A37813	UDP-N-acetylglucos
1141	49	10.6	146	2	T06471	core protein - gar	1214	49	10.6	411	2	S75327	lysothaphin - Syne
1142	49	10.6	154	2	C71379	probable ATPase, c	1215	49	10.6	419	1	S47692	hypothetical 43.8K
1143	49	10.6	157	2	S18651	variant surface an	1216	49	10.6	419	2	B91169	probable transport
1144	49	10.6	157	2	S58025	probable olfactory	1217	49	10.6	419	2	B86015	probable transport
1145	49	10.6	159	2	S77852	probable phenylala	1218	49	10.6	419	2	G70602	hypothetical prote
1146	49	10.6	160	2	S73261	plastoquinol-plast	1219	49	10.6	425	2	A64977	hypothetical prote
1147	49	10.6	163	2	D71062	hypothetical prote	1220	49	10.6	429	2	B87299	transporter, proba
1148	49	10.6	166	2	D82909	hypothetical prote	1221	49	10.6	431	1	E70699	probable pknA prot
1149	49	10.6	167	2	T11439	NADH2 dehydrogenas	1222	49	10.6	439	2	D72716	hypothetical prote
1150	49	10.6	167	2	B71553	hypothetical prote	1223	49	10.6	441	2	B82023	probable membrane-
1151	49	10.6	167	2	AE3204	hypothetical prote	1224	49	10.6	444	2	T24076	hypothetical prote
1152	49	10.6	169	2	B75490	hypothetical prote	1225	49	10.6	448	2	A70398	cell division prot
1153	49	10.6	170	2	H71937	3-dehydroquinat d	1226	49	10.6	450	2	E69934	conserved hypothet
1154	49	10.6	170	2	F90050	hypothetical prote	1227	49	10.6	458	2	AC1173	amino acid transpo
1155	49	10.6	172	2	T32259	hypothetical prote	1228	49	10.6	463	2	AD1530	amino acid transpo
1156	49	10.6	174	2	E90617	NADH dehydrogenase	1229	49	10.6	463	2	C86042	probable transport
1157	49	10.6	179	1	ERAD34	early E3 20.1K gly	1230	49	10.6	463	2	B91195	probable transport
1158	49	10.6	181	2	JX0247	serine proteinase	1231	49	10.6	463	2	H65166	probable transport
1159	49	10.6	185	2	T41299	hypothetical metal	1232	49	10.6	466	2	H69822	sodium-glutamate s
1160	49	10.6	195	2	AF2690	conserved hypothet	1233	49	10.6	466	2	G72603	nitrate reductase
1161	49	10.6	195	2	B97472	hypothetical prote	1234	49	10.6	469	1	AJECQ	glutamate-ammonia
1162	49	10.6	196	2	T49023	hypothetical prote	1235	49	10.6	469	2	A83356	hypothetical prote
1163	49	10.6	196	2	G87510	hypothetical prote	1236	49	10.6	469	2	C86074	glutamine syntheta
1164	49	10.6	203	2	E72345	endopeptidase Clp	1237	49	10.6	469	2	H91227	glutamine syntheta
1165	49	10.6	203	2	T32745	hypothetical prote	1238	49	10.6	473	2	T07548	photosystem II chl
1166	49	10.6	205	2	T14744	hypothetical prote	1239	49	10.6	475	2	T36342	probable glutamate
1167	49	10.6	207	2	D75341	conserved hypothet	1240	49	10.6	475	2	T06061	cellulase (EC 3.2.
1168	49	10.6	212	2	AC0074	probable tellurium	1241	49	10.6	476	2	H96802	probable amino aci
1169	49	10.6	217	2	B90765	hypothetical prote	1242	49	10.6	485	2	G65051	phosphotransferase
1170	49	10.6	224	2	AG1795	hypothetical prote	1243	49	10.6	485	2	C91075	hypothetical prote
1171	49	10.6	236	2	B81406	hypothetical prote	1244	49	10.6	485	2	B85920	hypothetical prote
1172	49	10.6	244	2	S07398	gamma-gliadin B pr	1245	49	10.6	491	2	B71957	ATP-dependent RNA
1173	49	10.6	255	4	S31866	Ig gamma-1 chain C	1246	49	10.6	492	2	G64550	uroporphyrinogen-I
1174	49	10.6	262	2	T48546	hypothetical prote	1247	49	10.6	493	2	A11224	uroporphyrinogen-I
1175	49	10.6	263	2	AB2559	transposase all806	1248	49	10.6	493	2	AC1578	T-cell surface gly
1176	49	10.6	276	2	S73410	hypothetical prote	1249	49	10.6	495	1	A26396	probable transcrip
1177	49	10.6	287	2	E83928	transcription regu	1250	49	10.6	496	2	F83124	LARI protein - hum
1178	49	10.6	288	2	AH0247	probable binding-p	1251	49	10.6	507	2	JG0165	cytochrome-c oxida
1179	49	10.6	300	2	G75436	conserved hypothet	1252	49	10.6	510	2	S55124	probable membrane
1180	49	10.6	308	1	QRECHB	chemotaxis protein	1253	49	10.6	516	2	C58892	cytochrome-c oxida
1181	49	10.6	308	2	C85802	hypothetical prote	1254	49	10.6	522	1	IKEC1	colicin E1 - Esche
1182	49	10.6	308	2	G90953	chemotaxis protein	1255	49	10.6	526	2	E65024	Hydrogenase-4 comp
1183	49	10.6	308	2	H82936	hpr serine/threoni	1256	49	10.6	535	2	D96586	hypothetical prote
1184	49	10.6	312	2	F87335	conserved hypothet	1257	49	10.6	542	2	C70732	probable integral
1185	49	10.6	322	2	AI2671	homoserine kinase	1258	49	10.6	553	1	H70786	probable dihydroli
1186	49	10.6	322	2	G97453	homoserine kinase	1259	49	10.6	555	2	S27163	alpha,alpha-trehal
1187	49	10.6	334	1	JC4280	carboxyl reductase	1260	49	10.6	557	2	AE3040	urocanase [importe
1188	49	10.6	334	2	T16772	hypothetical prote	1261	49	10.6	563	2	G98245	hutu gene homolog
1189	49	10.6	334	2	B87448	arginine N-succiny	1262	49	10.6	573	2	S28901	glutamate transpor
1190	49	10.6	335	2	T40292	glyceraldehyde 3-p	1263	49	10.6	582	2	PC5006	bps2 protein - Des
1191	49	10.6	337	1	QOECH3	probable dehydroge	1264	49	10.6	586	2	S22195	scaffolding protei
1192	49	10.6	337	2	C91029	probable PTS syste	1265	49	10.6	597	2	SS1212	BAK5 protein - bov
1193	49	10.6	337	2	D85873	probable PTS syste	1266	49	10.6	602	2	E70067	conserved hypothet
1194	49	10.6	345	2	T28026	hypothetical prote	1267	49	10.6	605	2	D83007	regulatory protein
1195	49	10.6	349	2	C86662	hypothetical prote	1268	49	10.6	616	2	AG2957	hypothetical prote
1196	49	10.6	352	2	A43113	chemokine (C-C) re	1269	49	10.6	616	2	G98325	probable c4-dicarb
1197	49	10.6	353	2	H88939	protein C05E4.13 [	1270	49	10.6				

979	50	10.8	606	2	S57552	hypothetical prote	1052	49.5	10.7	400	2	T46383	hypothetical prote
980	50	10.8	613	2	A56031	potassium channel	1053	49.5	10.7	401	2	D83022	hypothetical prote
981	50	10.8	610	2	E86194	hypothetical prote	1054	49.5	10.7	403	2	D75330	DNA polymerase pro
982	50	10.8	700	2	B81266	DNA topoisomerase	1055	49.5	10.7	424	2	D75330	probable beta-lact
983	50	10.8	749	1	B39898	phospholipase A2 (	1056	49.5	10.7	427	2	A49518	kallistatin precu
984	50	10.8	756	2	C46862	hypothetical prote	1057	49.5	10.7	430	1	S32570	malc protein - Sur
985	50	10.8	789	2	A82688	Na+/H+ antiporter	1058	49.5	10.7	430	2	A81356	hypothetical prote
986	50	10.8	789	2	H97469	probable NADH dehy	1059	49.5	10.7	430	2	A81726	hypothetical prote
987	50	10.8	810	1	F2WMBB	2a protein - broad	1060	49.5	10.7	432	2	H64383	Na+ transporter -
988	50	10.8	828	2	JC5807	trp3 protein - rat	1061	49.5	10.7	443	2	A80309	probable sugar tra
989	50	10.8	835	2	F70363	cation transportin	1062	49.5	10.7	469	2	T34645	hypothetical prote
990	50	10.8	836	2	C97525	clpA protein (Auj22	1063	49.5	10.7	469	2	S74825	probable Rieske ir
991	50	10.8	914	2	AD2744	ATP-dependent Clp	1064	49.5	10.7	476	1	VWUT4R	variant surface gl
992	50	10.8	876	2	T07101	lipoxigenase (EC 1	1065	49.5	10.7	476	2	B86829	multidrug transport
993	50	10.8	993	2	F97717	hypothetical prote	1066	49.5	10.7	478	2	T33942	hypothetical prote
994	50	10.8	1015	2	T15830	hypothetical prote	1067	49.5	10.7	502	2	T26256	hypothetical prote
995	50	10.8	1021	2	A86421	Receptor-like seri	1068	49.5	10.7	505	2	G90419	metabolite permeas
996	50	10.8	1022	2	F87635	AcRb/AcrD/AcrF fam	1069	49.5	10.7	508	2	H86474	hypothetical prote
997	50	10.8	1277	2	T14152	synaptic scaffold	1070	49.5	10.7	514	2	F87592	hypothetical prote
998	50	10.8	1338	2	T40993	protein kinase cek	1071	49.5	10.7	524	2	F85429	actin interacting
999	50	10.8	1381	2	T31083	paranodin - rat	1072	49.5	10.7	538	2	T40298	membrane transport
1000	50	10.8	1479	2	T42710	mannose receptor,	1073	49.5	10.7	538	2	A83018	probable sodium/hy
1001	50	10.8	1498	2	B97355	DNA segregation AT	1074	49.5	10.7	552	2	A51027	L-ascorbate oxidas
1002	50	10.8	1505	2	S26765	genome polyprotein	1075	49.5	10.7	553	2	B90153	2-isopropylmalate
1003	50	10.8	1524	2	S68553	surface layer prot	1076	49.5	10.7	556	2	T46842	K+-transporting AT
1004	50	10.8	1526	2	A95528	protein F27J15.14	1077	49.5	10.7	557	2	H97351	K+-transporting AT
1005	50	10.8	1687	2	S41742	calcium channel al	1078	49.5	10.7	559	2	C87307	hypothetical prote
1006	50	10.8	2109	2	T31352	hypothetical prote	1079	49.5	10.7	566	2	B82173	probable ABC trans
1007	50	10.8	2819	2	A90551	conserved hypotet	1080	49.5	10.7	579	2	S11027	L-ascorbate oxidas
1008	49.5	10.7	63	2	B90031	hypothetical prote	1081	49.5	10.7	583	2	T48473	amino acid transpo
1009	49.5	10.7	119	2	PH1544	Ig H chain V regio	1082	49.5	10.7	583	2	E83794	ABC transporter (A
1010	49.5	10.7	130	2	AD2901	hypothetical prote	1083	49.5	10.7	586	1	E89314	replication licens
1011	49.5	10.7	130	2	S67024	probable membrane	1084	49.5	10.7	660	2	B97853	NADH2 dehydrogenas
1012	49.5	10.7	150	2	F87507	conserved hypotet	1085	49.5	10.7	686	2	E71895	probable heavy-met
1013	49.5	10.7	160	2	C35542	ribosomal protein	1086	49.5	10.7	697	2	T13670	NADH2 dehydrogenas
1014	49.5	10.7	165	2	F97676	succinate dehydrog	1087	49.5	10.7	698	2	T12625	NADH2 dehydrogenas
1015	49.5	10.7	165	2	S50195	oleosin - rape	1088	49.5	10.7	699	2	T12673	NADH2 dehydrogenas
1016	49.5	10.7	171	2	S22194	hypothetical prote	1089	49.5	10.7	700	2	T32629	hypothetical prote
1017	49.5	10.7	172	2	T33644	apxIC protein - Ac	1090	49.5	10.7	701	2	T13056	NADH2 dehydrogenas
1018	49.5	10.7	197	2	AB2056	hypothetical prote	1091	49.5	10.7	701	2	T13587	NADH2 dehydrogenas
1019	49.5	10.7	214	2	D83881	siderophore (surfa	1092	49.5	10.7	702	2	T13058	NADH2 dehydrogenas
1020	49.5	10.7	218	2	AC1253	glycine betaine/ca	1093	49.5	10.7	702	2	T12624	NADH2 dehydrogenas
1021	49.5	10.7	218	2	A11615	glycine betaine/ca	1094	49.5	10.7	702	2	T13409	NADH2 dehydrogenas
1022	49.5	10.7	226	2	F87449	cell division prot	1095	49.5	10.7	703	2	T13074	NADH2 dehydrogenas
1023	49.5	10.7	244	2	E84885	hypothetical prote	1096	49.5	10.7	703	2	T13696	NADH2 dehydrogenas
1024	49.5	10.7	251	2	AF2281	hypothetical prote	1097	49.5	10.7	706	2	T12748	NADH2 dehydrogenas
1025	49.5	10.7	252	1	A34702	amphiregulin precu	1098	49.5	10.7	721	2	F82198	probable toxin sec
1026	49.5	10.7	255	2	H81302	probable membrane	1099	49.5	10.7	732	2	A83481	NADH2 dehydrogenas
1027	49.5	10.7	275	2	H90251	maltose transport	1100	49.5	10.7	734	1	DRR2N5	NADH2 dehydrogenas
1028	49.5	10.7	294	2	B83040	ribosomal protein	1101	49.5	10.7	738	2	S58612	NADH2 dehydrogenas
1029	49.5	10.7	295	2	T04483	probable ring fing	1102	49.5	10.7	740	2	B84741	hypothetical prote
1030	49.5	10.7	301	1	S10456	cytochrome c-type	1103	49.5	10.7	745	2	B84673	hypothetical prote
1031	49.5	10.7	302	2	F83392	hypothetical prote	1104	49.5	10.7	753	2	F69338	pyruvate, water di
1032	49.5	10.7	305	2	A10847	iron transport pro	1105	49.5	10.7	770	2	B56695	transducin-like en
1033	49.5	10.7	313	2	AH1672	malonyl CoA-acyl c	1106	49.5	10.7	776	2	S45495	isp4 protein - fis
1034	49.5	10.7	315	2	B98226	hypothetical prote	1107	49.5	10.7	788	1	I59282	diacylglycerol kin
1035	49.5	10.7	315	2	AF3060	conserved hypotet	1108	49.5	10.7	795	2	D82225	phenylalanyl-tRNA
1036	49.5	10.7	327	2	T32164	hypothetical prote	1109	49.5	10.7	822	2	T25866	outer membrane uah
1037	49.5	10.7	328	2	AD1916	alcohol dehydrogen	1110	49.5	10.7	826	2	AC0086	hypothetical prote
1038	49.5	10.7	330	2	H75353	probable nosk prot	1111	49.5	10.7	850	2	JC5700	Erbb kinase activa
1039	49.5	10.7	332	2	T33799	hypothetical prote	1112	49.5	10.7	875	2	T12794	hypothetical yomG
1040	49.5	10.7	334	2	T23444	hypothetical prote	1113	49.5	10.7	888	2	A54280	cell differentia
1041	49.5	10.7	341	2	C98304	probable oligopept	1114	49.5	10.7	914	1	JN0550	iodide peroxidase
1042	49.5	10.7	341	2	AB2979	hypothetical prote	1115	49.5	10.7	945	2	S77052	cation-transportin
1043	49.5	10.7	348	2	B48435	cysteine proteinas	1116	49.5	10.7	1039	2	T38447	tetratricopeptide
1044	49.5	10.7	360	2	B87286	conserved hypotet	1117	49.5	10.7	1069	2	D85383	hypothetical prote
1045	49.5	10.7	367	1	C69500	group II decarboxy	1118	49.5	10.7	1084	2	T15616	hypothetical prote
1046	49.5	10.7	368	1	QQBEHG	early nuclear anti	1119	49.5	10.7	1121	2	JC7329	WD-repeat protein
1047	49.5	10.7	372	1	D69442	conserved hypotet	1120	49.5	10.7	1132	2	T31107	telomerase reverse
1048	49.5	10.7	374	1	I39857	spore germination	1121	49.5	10.7	1163	2	A56097	arylphorin-binding
1049	49.5	10.7	374	2	T21513	hypothetical prote	1122	49.5	10.7	1195	2	S76592	5-methyltetrahydro
1050	49.5	10.7	380	1	TAGB	actinidin-(EC 3.4	1123	49.5	10.7	1354	2	AG0538	Rhs-family protein
1051	49.5	10.7	391	2	T43987	pp41, pol processi	1124	49.5	10.7	1461	2	E90696	hypothetical prote

833	50.5	11.0	442	2	S56057	heavy metal ion re	906	50	10.8	214	2	T10737	extensin-like cell
834	50.5	11.0	448	2	A83775	hypothetical prote	907	50	10.8	216	2	A11441	hypothetical prote
835	50.5	11.0	460	2	G85525	probable deaminase	908	50	10.8	219	2	T38019	uracil phosphorib
836	50.5	11.0	460	2	E90675	probable deaminase	909	50	10.8	232	2	S29001	G protein-coupled
837	50.5	11.0	470	2	T20851	hypothetical prote	910	50	10.8	236	2	T32473	hypothetical prote
838	50.5	11.0	471	2	D83546	probable amino aci	911	50	10.8	238	2	B64509	hypothetical prote
839	50.5	11.0	474	1	JH0790	lipoprotein lipase	912	50	10.8	250	2	S51206	cruxrhodopsin-1 -
840	50.5	11.0	507	2	T27627	hypothetical prote	913	50	10.8	255	2	A71351	probable cobalt AB
841	50.5	11.0	509	2	G81929	probable iron-upta	914	50	10.8	256	2	A81277	probable oxidoredu
842	50.5	11.0	510	2	T20850	hypothetical prote	915	50	10.8	259	2	C75151	oxidoreductase PAB
843	50.5	11.0	515	2	G75267	ABC transporter, p	916	50	10.8	265	2	D81315	hypothetical prote
844	50.5	11.0	517	2	S21042	cytochrome-c oxida	917	50	10.8	265	2	G97460	hypothetical prote
845	50.5	11.0	518	2	S34565	gene G protein - h	918	50	10.8	268	2	C83369	probable binding p
846	50.5	11.0	518	2	F70831	probable PPE prote	919	50	10.8	274	2	E75614	conserved hypotet
847	50.5	11.0	520	2	AD2383	Na+/H+-exchanging	920	50	10.8	293	2	T36063	probable integral
848	50.5	11.0	526	2	G83436	hypothetical prote	921	50	10.8	295	2	B85787	probable transposa
849	50.5	11.0	529	1	YRHU1	monophenol monooxy	922	50	10.8	295	2	T00315	transposase - Esch
850	50.5	11.0	543	2	T37570	WD repeat protein	923	50	10.8	296	2	I67971	transposase - Esch
851	50.5	11.0	543	2	S65462	glucose transport	924	50	10.8	296	2	D90398	conserved hypotet
852	50.5	11.0	544	2	AD1979	permease protein o	925	50	10.8	299	2	S50803	hypothetical prote
853	50.5	11.0	545	2	AC1914	hypothetical prote	926	50	10.8	299	2	S50803	hypothetical prote
854	50.5	11.0	546	2	B40407	sterol carrier pro	927	50	10.8	304	2	A72596	hypothetical prote
855	50.5	11.0	563	2	S32156	mandelonitrile lya	928	50	10.8	308	2	S22928	hypothetical prote
856	50.5	11.0	577	2	T52608	probable nitrate t	929	50	10.8	312	2	S72525	ubiquinol-cytochro
857	50.5	11.0	584	2	S40013	hypothetical prote	930	50	10.8	332	2	B87666	pectinesterase (EC
858	50.5	11.0	586	2	F84663	probable nitrate t	931	50	10.8	332	2	C84061	homoserine kinase
859	50.5	11.0	595	2	AH2718	aspartyl-CRNA synt	932	50	10.8	333	2	T36036	cysteine synthase
860	50.5	11.0	595	2	D97500	aspartyl)-tRNA syn	933	50	10.8	337	2	AG0802	ferrichrome ABC tr
861	50.5	11.0	608	2	T76192	hypothetical prote	934	50	10.8	341	2	D48435	probable integral
862	50.5	11.0	684	2	T25603	hypothetical prote	935	50	10.8	348	2	E86818	probable semialdeh
863	50.5	11.0	688	2	H96681	protein FlE22.10 [	936	50	10.8	348	2	E86818	cysteine proteinase
864	50.5	11.0	704	2	F87706	prolyl oligopeptid	937	50	10.8	357	2	D83685	dehydrogenase [imp
865	50.5	11.0	712	2	AD2721	H+ translocating p	938	50	10.8	357	2	T09261	dehydrogenase [imp
866	50.5	11.0	714	2	H97502	h+ translocating p	939	50	10.8	372	2	S20056	nicotinate-nucleot
867	50.5	11.0	731	2	E82922	phosphate transpor	940	50	10.8	375	2	T25089	JUN kinase-activat
868	50.5	11.0	736	2	C82821	bacteriophytochrom	941	50	10.8	380	2	A71390	para-hydroxybenzoa
869	50.5	11.0	745	2	C97599	cell division proc	942	50	10.8	388	2	D69468	ubiquinol-cytochro
870	50.5	11.0	819	2	F87708	hypothetical prote	943	50	10.8	388	2	AF0183	ammonium transport
871	50.5	11.0	827	2	A95877	two-component regu	944	50	10.8	393	2	S61659	probable exported
872	50.5	11.0	908	2	A10327	protein kinase TMK	945	50	10.8	397	2	E91296	KTR1 protein - yea
873	50.5	11.0	942	1	JQ1674	hypothetical prote	946	50	10.8	407	2	F70318	probable thymidine
874	50.5	11.0	962	2	T05845	cell surface glyco	947	50	10.8	414	1	E70708	hypothetical prote
875	50.5	11.0	1163	1	RWHU1C	hypothetical prote	948	50	10.8	420	2	A82856	cytochrome P450 Rv
876	50.5	11.0	1188	2	T20333	hypothetical prote	949	50	10.8	434	2	A12379	conserved hypotet
877	50.5	11.0	1265	2	T47626	structural mainten	950	50	10.8	435	2	G86907	hypothetical prote
878	50.5	11.0	1317	2	T03748	apoptosis associat	951	50	10.8	440	1	S56606	D-alanyl-D-alanine
879	50.5	11.0	1345	2	T44204	capsid protein U57	952	50	10.8	440	1	G86137	thymidine phosphor
880	50.5	11.0	1345	2	T44017	major capsid prote	953	50	10.8	449	2	H69862	Na+-transporting A
881	50.5	11.0	1400	2	B70963	hypothetical prote	954	50	10.8	457	1	A28468	chromogranin A pre
882	50.5	11.0	1447	1	VGIHE3	E2 glycoprotein pr	955	50	10.8	457	2	A53669	streptogrin C (E
883	50.5	11.0	1447	1	VGIHE2	E2 glycoprotein pr	956	50	10.8	460	2	JL0145	interleukin-6 rece
884	50.5	11.0	1449	1	A43573	E2 glycoprotein pr	957	50	10.8	473	1	F2R244	photosystem II chl
885	50.5	11.0	1449	1	VGIHFS	E2 glycoprotein pr	958	50	10.8	473	1	F2SP44	photosystem II chl
886	50.5	11.0	1577	2	T15851	hypothetical prote	959	50	10.8	473	2	T08998	photosystem II pro
887	50.5	11.0	1672	2	C81675	polymorphic membra	960	50	10.8	476	2	AC2306	hypothetical prote
888	50.5	11.0	1921	2	T13827	kinesin-73 - fruit	961	50	10.8	489	2	A11639	multidrug-efflux t
889	50.5	11.0	89	2	H83795	hypothetical prote	962	50	10.8	489	2	C70940	probable cobQ prot
890	50.5	10.8	100	2	A12298	cobalt transport p	963	50	10.8	498	2	F98149	hypothetical prote
891	50.5	10.8	102	2	A75417	hypothetical prote	964	50	10.8	514	2	C49507	potassium channel
892	50.5	10.8	121	2	B72546	hypothetical prote	965	50	10.8	516	2	S39686	Na+-dependent symp
893	50.5	10.8	138	2	JC1342	phospholipase A2 (	966	50	10.8	532	2	JC1392	monophenol monooxy
894	50.5	10.8	147	2	S70109	hypothetical prote	967	50	10.8	533	2	AE3138	hypothetical prote
895	50.5	10.8	150	2	G72660	hypothetical prote	968	50	10.8	538	2	C83284	probable biotin-de
896	50.5	10.8	170	2	B86942	hypothetical prote	969	50	10.8	538	2	C86976	PPE-family protein
897	50.5	10.8	175	2	T11179	NADH2 dehydrogenas	970	50	10.8	539	2	C83758	cephalosporin acyl
898	50.5	10.8	175	2	AE1149	hypothetical prote	971	50	10.8	542	2	S50361	probable membrane
899	50.5	10.8	186	2	E82625	outer membrane pro	972	50	10.8	545	2	T18694	hypothetical prote
900	50.5	10.8	195	2	T39603	BAG-family molecucl	973	50	10.8	545	2	T39499	conserved hypotet
901	50.5	10.8	203	2	D81934	probable periplasm	974	50	10.8	545	2	D83440	probable sulfate t
902	50.5	10.8	203	2	F81171	cryptic protein NM	975	50	10.8	588	2	T25248	hypothetical prote
903	50.5	10.8	211	2	A47686	bacteriorhodopsin-	976	50	10.8	598	2	S66669	potassium channel
904	50.5	10.8	211	2	AC0268	probable exported	977	50	10.8	602	2	A49507	potassium channel
905	50.5	10.8	213	2	G75521	ABC transporter, A	978	50	10.8	602	2	JH0166	potassium voltage-

687	51	11.1	279	2	T22051	hypothetical prote	760	50.5	11.0	173	2	S59864	TRAP-like protein
688	51	11.1	282	2	E64063	hypothetical prote	761	50.5	11.0	201	1	IMPSB	immunity protein -
689	51	11.1	282	2	A41025	asparillopepin I	762	50.5	11.0	204	2	E83036	hypothetical prote
690	51	11.1	285	2	T15498	hypothetical prote	763	50.5	11.0	208	2	F71314	probable transcrip
691	51	11.1	295	2	F90938	hypothetical prote	764	50.5	11.0	217	2	I51062	MHC class II beta
692	51	11.1	295	2	B85664	transposase for IS	765	50.5	11.0	224	2	T34686	probable integral
693	51	11.1	295	2	D90801	hypothetical prote	766	50.5	11.0	227	2	T12797	immunity protein d
694	51	11.1	295	2	B85613	probable transposa	767	50.5	11.0	228	2	C28551	hypothetical prote
695	51	11.1	309	2	AF0746	motility protein B	768	50.5	11.0	231	2	H81698	hypothetical prote
696	51	11.1	321	1	A55090	cathepsin O (EC 3.	769	50.5	11.0	233	2	JH0372	42K surface glycop
697	51	11.1	328	1	S64306	hypothetical prote	770	50.5	11.0	234	2	E95360	hypothetical prote
698	51	11.1	345	2	AG0645	spermidine/putresc	771	50.5	11.0	240	1	TOEC34	transposase - Esch
699	51	11.1	355	2	E96785	protein F10A5_28 [	772	50.5	11.0	247	2	I51060	MHC class II beta
700	51	11.1	357	2	A71523	probable chorismat	773	50.5	11.0	247	2	I51059	MHC class II beta
701	51	11.1	361	2	A45211	prostaglandin E re	774	50.5	11.0	249	2	S75671	hypothetical prote
702	51	11.1	362	2	A53058	prostaglandin F2-a	775	50.5	11.0	249	2	H95256	ABC transporter, p
703	51	11.1	364	2	S65009	prostaglandin E re	776	50.5	11.0	250	2	T09160	proteasome subunit
704	51	11.1	365	2	A42414	prostaglandin E re	777	50.5	11.0	252	2	F70711	probable membranep
705	51	11.1	372	2	S75587	H+/Ca2+ exchanging	778	50.5	11.0	253	2	A98122	hypothetical prote
706	51	11.1	375	2	T03256	GTP-binding protei	779	50.5	11.0	255	2	JN0829	3alpha-hydroxyster
707	51	11.1	377	2	T04086	GTP binding protei	780	50.5	11.0	258	2	A69805	hypothetical prote
708	51	11.1	377	2	T16985	GTP-binding protei	781	50.5	11.0	260	2	F82954	probable short-cha
709	51	11.1	379	2	AB2423	hypothetical prote	782	50.5	11.0	264	2	D87504	hypothetical prote
710	51	11.1	384	2	A69622	ferrichrome ABC tr	783	50.5	11.0	286	2	E86844	shikimate 5-dehydr
711	51	11.1	394	2	B85535	probable transport	784	50.5	11.0	288	2	F85818	hypothetical prote
712	51	11.1	394	2	F90684	probable transport	785	50.5	11.0	293	2	A83623	hypothetical prote
713	51	11.1	402	2	B82491	NupC family protei	786	50.5	11.0	296	2	A85841	probable transposa
714	51	11.1	404	2	T39270	conserved hypothet	787	50.5	11.0	296	2	D91284	hypothetical prote
715	51	11.1	409	2	G90491	conserved hypothet	788	50.5	11.0	296	2	F90868	hypothetical prote
716	51	11.1	416	2	T14554	calreticulin - bee	789	50.5	11.0	296	2	D90995	hypothetical prote
717	51	11.1	418	2	S31124	hypothetical prote	790	50.5	11.0	296	2	E91020	hypothetical prote
718	51	11.1	421	2	B82062	conserved hypothet	791	50.5	11.0	296	2	A91132	hypothetical prote
719	51	11.1	423	2	AB0054	probable Na+ depen	792	50.5	11.0	296	2	F91111	hypothetical prote
720	51	11.1	435	2	E71350	probable aspartate	793	50.5	11.0	296	2	G90998	hypothetical prote
721	51	11.1	439	2	S58327	cobalt accumulatio	794	50.5	11.0	296	2	T00240	transposase - Esch
722	51	11.1	439	2	T18898	hypothetical prote	795	50.5	11.0	296	2	B90837	hypothetical prote
723	51	11.1	440	2	AD1073	thymidine phosphor	796	50.5	11.0	296	2	C91065	hypothetical prote
724	51	11.1	449	2	C86496	hypothetical prote	797	50.5	11.0	296	2	H90779	hypothetical prote
725	51	11.1	449	2	D72127	hypothetical prote	798	50.5	11.0	296	2	C90906	hypothetical prote
726	51	11.1	449	2	A81544	hypothetical prote	799	50.5	11.0	296	2	A99972	hypothetical prote
727	51	11.1	450	2	AB1420	PTS cellobiose-spe	800	50.5	11.0	297	2	T09542	endonuclease G (EC
728	51	11.1	450	2	AC1795	PTS cellobiose-spe	801	50.5	11.0	297	2	T45436	hypothetical membr
729	51	11.1	458	1	YTB5Y8	tetracycline resis	802	50.5	11.0	302	2	S02728	actinidain (EC 3.4
730	51	11.1	460	2	S06469	photosystem II chl	803	50.5	11.0	302	2	S60955	probable membrane
731	51	11.1	466	2	E84132	aminopeptidase BH3	804	50.5	11.0	313	2	AH1300	malonyl CoA-acyl c
732	51	11.1	468	2	A69468	ammonium transport	805	50.5	11.0	314	2	F86928	34 kDa antigen [im
733	51	11.1	485	2	A72006	arginine/ornithine	806	50.5	11.0	317	2	T27994	hypothetical prote
734	51	11.1	514	2	A96671	Ammonium transport	807	50.5	11.0	324	2	A86839	conserved hypothet
735	51	11.1	516	2	T09859	cytochrome-c oxida	808	50.5	11.0	327	2	S61982	probable membrane
736	51	11.1	525	2	T00459	hypothetical prote	809	50.5	11.0	332	2	S77386	nitrate transport
737	51	11.1	528	2	T22583	hypothetical prote	810	50.5	11.0	346	2	C71390	NADH2 dehydrogenas
738	51	11.1	531	2	T12406	cytochrome-c oxida	811	50.5	11.0	351	2	A69808	H+/Ca2+ exchanger
739	51	11.1	560	2	T51485	sugar transporter-	812	50.5	11.0	355	1	BVECMG	UDP-N-acetylglucos
740	51	11.1	566	2	T07611	aconitate hydratase	813	50.5	11.0	355	2	F85491	hypothetical prote
741	51	11.1	635	1	A64162	cytochrome c-type	814	50.5	11.0	355	2	F90640	hypothetical prote
742	51	11.1	639	2	JQ0607	glucan 1,4-alpha-g	815	50.5	11.0	361	2	F87286	cation efflux fani
743	51	11.1	639	2	A68602	unknown protein [i	816	50.5	11.0	362	2	JC7559	sphingosine 1-phos
744	51	11.1	745	1	A70458	phosphoribosylform	817	50.5	11.0	364	2	H70776	hypothetical prote
745	51	11.1	749	1	A93329	phospholipase A2 (	818	50.5	11.0	377	2	B53044	geranylgeranyl-dip
746	51	11.1	754	2	S37403	transcription fact	819	50.5	11.0	379	2	T45768	protein phosphatas
747	51	11.1	770	2	T50308	probable tranelati	820	50.5	11.0	382	2	H90500	glycolate oxidase
748	51	11.1	778	2	E97224	ATP-dependent Lon	821	50.5	11.0	398	2	S75202	hypothetical prote
749	51	11.1	854	2	T23837	hypothetical prote	822	50.5	11.0	399	2	T26257	hypothetical prote
750	51	11.1	862	2	T46289	hypothetical prote	823	50.5	11.0	406	2	T27947	hypothetical prote
751	51	11.1	873	2	T16288	hypothetical prote	824	50.5	11.0	407	2	E70309	hypothetical prote
752	51	11.1	887	2	T01113	translation initia	825	50.5	11.0	408	2	T29949	hypothetical prote
753	51	11.1	967	2	A30325	membrane alanyl am	826	50.5	11.0	410	2	JC7584	basic helix-loop-h
754	51	11.1	1075	2	D70568	hypothetical prote	827	50.5	11.0	411	2	AG3003	conserved hypothet
755	51	11.1	1325	2	A64905	ydek protein - Esc	828	50.5	11.0	411	2	B98280	hypothetical prote
756	51	11.1	1790	1	D27772	vitellogenin precu	829	50.5	11.0	421	2	D70868	probable lipQ prot
757	50.5	11.0	137	2	D75337	hypothetical prote	830	50.5	11.0	424	2	A71846	glycinamide ribonu
758	50.5	11.0	141	2	E72580	hypothetical prote	831	50.5	11.0	424	2	B64672	glycinamide ribonu
759	50.5	11.0	155	2	T22027	hypothetical prote	832	50.5	11.0	441	2	AF0411	probable chloride

541	52	11.3	417	2	E69804	multidrug resistan	614	51.5	11.2	410	2	S45894	regulatory protein
542	52	11.3	457	2	S39079	puff C-8 protein -	615	51.5	11.2	429	2	F87038	probable membrane
543	52	11.3	469	2	D81017	chloride channel p	616	51.5	11.2	438	2	A83037	probable MFS trans
544	52	11.3	470	2	C70641	hypothetical prote	617	51.5	11.2	450	2	C96704	unknown protein, 2
545	52	11.3	491	2	S75449	hypothetical prote	618	51.5	11.2	451	2	F75177	tryptophan synthas
546	52	11.3	502	2	G87433	conserved hypothet	619	51.5	11.2	474	1	A40570	lipoprotein lipase
547	52	11.3	502	2	T29729	hypothetical prote	620	51.5	11.2	478	1	C42790	cystathionine beta
548	52	11.3	526	2	H85891	hydrogenase 4 memb	621	51.5	11.2	478	2	T30763	hypothetical prote
549	52	11.3	526	2	D91047	hydrogenase 4 memb	622	51.5	11.2	478	2	T32476	probable protein-t
550	52	11.3	530	2	D87255	apolipoprotein N-a	623	51.5	11.2	481	2	B82130	pyruvate kinase II
551	52	11.3	534	2	T27054	hypothetical prote	624	51.5	11.2	493	2	T21445	hypothetical prote
552	52	11.3	544	2	T17422	halogenase-like pr	625	51.5	11.2	509	2	G82409	glyceraldehyde 3-p
553	52	11.3	548	2	C82698	electron transfer	626	51.5	11.2	513	2	T34546	hypothetical prote
554	52	11.3	553	2	S75892	probable glycerol-	627	51.5	11.2	525	2	A70735	probable guaA prot
555	52	11.3	567	2	H87370	major facilitator	628	51.5	11.2	531	2	D69655	PTS system, arbuti
556	52	11.3	573	2	A33533	cell surface glyco	629	51.5	11.2	534	1	JU0274	cell fusion glycop
557	52	11.3	579	2	A64100	inner membrane cop	630	51.5	11.2	536	2	D81700	CTP synthase TC045
558	52	11.3	635	2	H69626	PTS fructose-speci	631	51.5	11.2	536	2	F85697	hypothetical prote
559	52	11.3	706	2	H81943	probable polyribon	632	51.5	11.2	536	2	D64865	probable Na+/H+-ex
560	52	11.3	707	2	C81161	polyribonucleotide	633	51.5	11.2	536	2	F90839	hypothetical prote
561	52	11.3	733	2	F82965	hypothetical prote	634	51.5	11.2	540	1	JU0470	site-specific DNA-
562	52	11.3	738	2	S37876	glutamine-rich pro	635	51.5	11.2	541	1	A70022	multidrug-efflux t
563	52	11.3	773	2	AH2061	hypothetical prote	636	51.5	11.2	541	2	JN0511	heat shock protein
564	52	11.3	823	2	A96737	hypothetical prote	637	51.5	11.2	547	2	T46059	MAP kinase - Arabi
565	52	11.3	840	2	T21333	hypothetical prote	638	51.5	11.2	549	2	T51099	cell fusion glycop
566	52	11.3	869	2	A95156	conserved hypothet	639	51.5	11.2	550	1	E48556	conserved hypothet
567	52	11.3	878	2	D98022	conserved hypothet	640	51.5	11.2	558	2	C72391	interferon alpha r
568	52	11.3	906	2	AE2533	hypothetical prote	641	51.5	11.2	560	2	T27387	cystathionine beta
569	52	11.3	1016	2	T00375	hypothetical prote	642	51.5	11.2	561	1	A42790	probable membrane
570	52	11.3	1017	2	T37201	hypothetical prote	643	51.5	11.2	623	2	T35377	transketolase (EC
571	52	11.3	1106	2	A97647	cation efflux syst	644	51.5	11.2	666	2	AF0815	transketolase (EC
572	52	11.3	1106	2	AG2870	Acr family transpo	645	51.5	11.2	667	1	A48660	transketolase 2 is
573	52	11.3	1146	2	T09112	probable sensor ki	646	51.5	11.2	667	2	G91044	transketolase 2 is
574	52	11.3	1146	2	A82174	sensory box sensor	647	51.5	11.2	667	2	B85889	NADH2 dehydrogenas
575	52	11.3	1146	2	C97196	probable membrane	648	51.5	11.2	682	2	T12715	hypothetical prote
576	52	11.3	1957	2	S68453	sodium channel pro	649	51.5	11.2	724	2	T19601	hypothetical prote
577	52	11.3	2139	2	A44667	voltage-dependent	650	51.5	11.2	726	2	T31287	hypothetical prote
578	52	11.3	2220	2	A45290	calcium channel pr	651	51.5	11.2	763	2	AI3443	Na+/H+ antiporter
579	52	11.3	3429	2	T13853	hypothetical prote	652	51.5	11.2	765	2	B75288	phenylalanyl-tRNA
580	51.5	11.2	116	2	A83693	transcription regu	653	51.5	11.2	795	2	AE0705	hypothetical prote
581	51.5	11.2	122	1	PSABA	phospholipase A2 (	654	51.5	11.2	829	2	T29372	hypothetical prote
582	51.5	11.2	131	2	C72563	hypothetical prote	655	51.5	11.2	846	2	T27282	cfaC protein precu
583	51.5	11.2	146	2	S42570	flavodoxin - Desul	656	51.5	11.2	869	2	C56617	E2 glycoprotein pr
584	51.5	11.2	167	2	H86784	WSP29-like phospho	657	51.5	11.2	1451	1	JQ1719	hypothetical prote
585	51.5	11.2	172	2	F75491	conserved hypothet	658	51.5	11.2	1755	2	T51532	hypothetical prote
586	51.5	11.2	206	1	I40173	orotate phosphorib	659	51.5	11.2	1784	2	T43167	sodium channel pro
587	51.5	11.2	209	2	T00733	hypothetical prote	660	51.5	11.2	2301	1	GNNYTN	genome polyprotein
588	51.5	11.2	212	1	A49436	dual specificity p	661	51.5	11.2	2303	1	GNNYTM	genome polyprotein
589	51.5	11.2	222	2	H64495	cobalamin biosynth	662	51	11.1	89	2	AH3403	CT001 hypothetical
590	51.5	11.2	270	2	A29934	pancreatic elastas	663	51	11.1	93	2	A86491	conserved hypothet
591	51.5	11.2	276	2	A70425	hypothetical prote	664	51	11.1	93	2	F72130	hypothetical prote
592	51.5	11.2	282	2	AC2294	hypothetical prote	665	51	11.1	95	2	AG2439	hypothetical prote
593	51.5	11.2	289	2	G97192	oligopeptide ABC-t	666	51	11.1	97	2	C75415	hypothetical prote
594	51.5	11.2	299	2	B95939	probable spermidin	667	51	11.1	106	2	A72588	hypothetical prote
595	51.5	11.2	299	2	H97884	hypothetical prote	668	51	11.1	152	2	H95153	conserved hypothet
596	51.5	11.2	312	2	B69170	UDP-N-acetylmuram	669	51	11.1	173	2	AF2518	hypothetical prote
597	51.5	11.2	313	2	S75329	hypothetical prote	670	51	11.1	168	2	T15651	hypothetical prote
598	51.5	11.2	314	2	T21971	hypothetical prote	671	51	11.1	201	2	E75039	multiple antibioti
599	51.5	11.2	319	2	T02691	glycosyl protein gl	672	51	11.1	202	2	A81441	probable orotate p
600	51.5	11.2	342	2	T16806	hypothetical prote	673	51	11.1	204	2	A82389	conserved hypothet
601	51.5	11.2	355	2	S76667	hypothetical prote	674	51	11.1	212	2	I67437	cysteine proteinas
602	51.5	11.2	364	2	G82734	acetylornithine de	675	51	11.1	221	2	S75146	hypothetical prote
603	51.5	11.2	366	2	F53488	prostaglandin F2 a	676	51	11.1	229	2	E85806	hypothetical prote
604	51.5	11.2	366	2	S51281	F2-alpha receptor	677	51	11.1	229	2	D90958	hypothetical prote
605	51.5	11.2	370	2	AH1485	fructose-specific	678	51	11.1	240	2	T02059	GRP-binding regula
606	51.5	11.2	370	2	AI1124	fructose-specific	679	51	11.1	246	2	S26826	histone H1 - maize
607	51.5	11.2	376	2	A75381	peptide ABC transp	680	51	11.1	246	2	T28166	hypothetical prote
608	51.5	11.2	380	2	D83174	probable acetylpol	681	51	11.1	261	2	A71192	probable glucose 1
609	51.5	11.2	381	2	A35300	G protein-coupled	682	51	11.1	263	2	AG2280	glutathione S-tran
610	51.5	11.2	381	2	F87553	aminotransferase,	683	51	11.1	264	2	G96978	uncharacterized co
611	51.5	11.2	382	2	G84971	ompF-like porin [i	684	51	11.1	265	2	B81229	phosphatidate cyti
612	51.5	11.2	383	2	I53870	Edg-1 orphan recep	685	51	11.1	265	2	A82000	phosphatidate cyti
613	51.5	11.2	390	2	C95954	hypothetical prote	686	51	11.1	268	2	S03328	embryonic abundant



395	53	11.5	385	2	B86024	probable membrane	468	52.5	11.4	409	2	T47644	protein phosphatas
396	53	11.5	385	2	S47733	yh1u protein precu	469	52.5	11.4	410	2	B48585	transcription fact
397	53	11.5	386	2	A26017	patatin T5 precurs	470	52.5	11.4	421	2	T35515	hypothetical prote
398	53	11.5	403	2	E69873	cell-division prot	471	52.5	11.4	422	2	JE0239	lin-10 protein - r
399	53	11.5	405	2	S61551	breast-regressing	472	52.5	11.4	422	2	E82904	hypothetical prote
400	53	11.5	409	2	F83493	probable MFS trans	473	52.5	11.4	429	2	AF0681	probable voltage g
401	53	11.5	418	2	H82087	NupC family protei	474	52.5	11.4	429	2	S30049	transcription fact
402	53	11.5	426	2	B82712	ATP-dependent Cip	475	52.5	11.4	452	2	G95356	probable oxidoredu
403	53	11.5	438	2	G87675	arylesterase-relat	476	52.5	11.4	500	2	H70629	probable AMINOPEPT
404	53	11.5	447	2	H86534	hypothetical prote	477	52.5	11.4	514	2	T21286	hypothetical prote
405	53	11.5	447	2	H72089	hypothetical prote	478	52.5	11.4	523	2	S53401	probable membrane
406	53	11.5	463	2	B81580	hypothetical prote	479	52.5	11.4	533	1	YRMSCS	monophenol monooxy
407	53	11.5	469	1	AJF8QT	glutamate-ammonia	480	52.5	11.4	542	2	AH2191	hypothetical prote
408	53	11.5	469	2	AI0949	glutamate syntheta	481	52.5	11.4	542	2	AI3564	hypothetical membr
409	53	11.5	469	2	S23899	glutamate-ammonia	482	52.5	11.4	546	2	B32688	beta-galactosidase
410	53	11.5	471	2	S78347	photosystem II chl	483	52.5	11.4	549	2	G91178	cytoplasmic trehal
411	53	11.5	515	2	B84406	TRK potassium upta	484	52.5	11.4	549	2	H86024	cytoplasmic trehal
412	53	11.5	581	2	T38501	hypothetical prote	485	52.5	11.4	549	2	S47739	probable alpha,alp
413	53	11.5	586	2	T20036	hypothetical prote	486	52.5	11.4	572	2	A55676	excitatory amino a
414	53	11.5	588	2	AC2276	oligopeptide bindi	487	52.5	11.4	652	2	AH2245	thiamin biosynthes
415	53	11.5	605	2	E69153	cadmium eflux ATP	488	52.5	11.4	657	1	A64079	2',3'-cyclic-nucle
416	53	11.5	610	2	A55939	dihydrolipoamide S	489	52.5	11.4	686	2	T06700	hypothetical prote
417	53	11.5	618	2	AI3303	hypothetical prote	490	52.5	11.4	699	2	T12170	NADH2 dehydrogenas
418	53	11.5	637	2	T49099	dihydrolipoamide S	491	52.5	11.4	699	2	T12172	NADH2 dehydrogenas
419	53	11.5	653	2	A83154	probable choline t	492	52.5	11.4	699	2	T12173	phenylalanine-trNA
420	53	11.5	656	2	T52064	dnaU-like protein	493	52.5	11.4	795	1	SYECFB	phenylalanine-trNA
421	53	11.5	720	2	D86278	hypothetical prote	494	52.5	11.4	795	2	H85779	phenylalanine trNA
422	53	11.5	727	2	T23999	hypothetical prote	495	52.5	11.4	795	2	D90931	glucose dehydrogen
423	53	11.5	776	2	T02584	probable protein k	496	52.5	11.4	803	2	F83360	malate synthase, p
424	53	11.5	1005	2	B82969	sarcosine oxidase	497	52.5	11.4	826	2	E90289	conserved hypothet
425	53	11.5	1070	2	JC4593	protein-tyrosine k	498	52.5	11.4	883	2	AE0207	hypothetical prote
426	53	11.5	1162	2	E84431	probable Na+/H+ an	499	52.5	11.4	977	2	T41289	hypothetical prote
427	53	11.5	1176	2	E58345	protein tyrosine p	500	52.5	11.4	1011	2	T40851	hypothetical prote
428	53	11.5	1240	1	DJBE21	DNA-directed DNA p	501	52.5	11.4	1205	2	T18517	procollagen N-endo
429	53	11.5	1250	2	T00454	hypothetical prote	502	52.5	11.4	1225	1	S24284	E2 glycoprotein pr
430	53	11.5	1305	2	T23314	hypothetical prote	503	52.5	11.4	1225	2	A36607	E2 glycoprotein -
431	53	11.5	1326	2	B58395	secretory phosphol	504	52.5	11.4	1345	1	VCBEHG	major capsid prote
432	53	11.5	1331	2	S05011	calcium channel al	505	52.5	11.4	1453	2	S41453	spike protein - ca
433	53	11.5	1465	2	A56395	secretory phosphol	506	52.5	11.4	1541	2	T30227	pipicolate-incorpo
434	53	11.5	1529	2	T16779	hypothetical prote	507	52.5	11.4	1544	2	T29482	hypothetical prote
435	53	11.5	2143	2	JH0427	voltage-dependent	508	52.5	11.4	2285	1	G02434	DNA-directed DNA p
436	53	11.5	2166	2	S11339	calcium channel pr	509	52	11.3	119	2	D64611	hypothetical prote
437	53	11.5	2171	2	S05054	calcium channel al	510	52	11.3	122	2	F75351	hypothetical prote
438	53	11.5	2599	2	A96616	unknown protein F1	511	52	11.3	148	2	D64356	conserved hypothet
439	52.5	11.4	71	2	I50439	vitellogenin III -	512	52	11.3	160	2	G95113	regulatory protein
440	52.5	11.4	78	2	G64333	ribosomal protein	513	52	11.3	160	2	H97982	regulatory protein
441	52.5	11.4	159	2	E85360	hypothetical prote	514	52	11.3	175	2	AE1508	hypothetical prote
442	52.5	11.4	165	2	C72116	hypothetical prote	515	52	11.3	202	2	JC4635	tumor-associated L
443	52.5	11.4	210	2	A83516	probable outer mem	516	52	11.3	207	2	T45600	hypothetical prote
444	52.5	11.4	219	2	F73402	probable competenc	517	52	11.3	219	2	G97271	probable phosphogl
445	52.5	11.4	219	2	AC1881	hypothetical prote	518	52	11.3	235	2	E82173	pseudouridine synt
446	52.5	11.4	244	2	S29982	class II histocomp	519	52	11.3	238	2	C82866	conjugal transfer
447	52.5	11.4	245	2	S29980	class II histocomp	520	52	11.3	260	2	I56559	neurospain - mouse
448	52.5	11.4	256	2	S14518	chlorophyll a/b-bi	521	52	11.3	262	2	B81200	conserved hypothet
449	52.5	11.4	257	2	S29981	class II histocomp	522	52	11.3	265	2	D83761	hypothetical prote
450	52.5	11.4	285	1	A43556	homeotic protein H	523	52	11.3	291	2	B75618	chromosome partiti
451	52.5	11.4	289	2	E64330	dihydrodipicolinat	524	52	11.3	295	2	E85661	probable transposa
452	52.5	11.4	296	2	S09261	probable transposa	525	52	11.3	297	2	T47857	myb protein-like -
453	52.5	11.4	301	2	B64189	glycine cleavage s	526	52	11.3	310	2	S46239	ribosome-inactivat
454	52.5	11.4	309	2	A87564	membrane protein,	527	52	11.3	310	2	T32006	hypothetical prote
455	52.5	11.4	310	2	C39778	tagatose-6-phospha	528	52	11.3	320	2	AI2305	hypothetical prote
456	52.5	11.4	310	2	T31125	hypothetical prote	529	52	11.3	327	2	AE2608	transcription regu
457	52.5	11.4	322	2	AF1031	hypothetical prote	530	52	11.3	327	2	G97390	arac family transc
458	52.5	11.4	332	2	C72310	conserved hypothet	531	52	11.3	359	2	A43532	B-cell surface ant
459	52.5	11.4	334	2	D81217	hypothetical prote	532	52	11.3	364	2	B71139	hypothetical prote
460	52.5	11.4	342	2	T33950	cysteine proteinas	533	52	11.3	372	2	B64819	probable membrane
461	52.5	11.4	342	2	C48435	hypothetical prote	534	52	11.3	372	2	B85591	hypothetical prote
462	52.5	11.4	356	2	D84280	RNA helicase RH18	535	52	11.3	372	2	G90740	hypothetical prote
463	52.5	11.4	360	2	T51344	prostaglandin F re	536	52	11.3	375	2	S47704	probable transport
464	52.5	11.4	366	2	A49877	amino acid transpo	537	52	11.3	375	2	F91173	probable transport
465	52.5	11.4	377	2	C69758	hypothetical prote	538	52	11.3	379	2	F86019	hypothetical prote
466	52.5	11.4	394	2	B86507	hypothetical prote	539	52	11.3	397	2	F83152	conserved hypothet
467	52.5	11.4	394	2	B81554	hypothetical prote	540	52	11.3	397	2	B70048	conserved hypothet

249	54.5	11.8	185	2	T51844	RING-H2 finger pro	322	54	11.7	909	2	T00009	probable primase (
250	54.5	11.8	204	2	AC1961	ATP-dependent Clp	323	54	11.7	967	2	I40889	sarcosine oxidase
251	54.5	11.8	226	2	S76020	endopeptidase Clp	324	54	11.7	993	2	A38437	probable homeotic
252	54.5	11.8	255	2	F86203	hypothetical prote	325	54	11.7	1072	2	T50949	verprolin related
253	54.5	11.8	269	2	T19947	hypothetical prote	326	54	11.7	1222	2	G72614	probable reverse g
254	54.5	11.8	276	2	AC1838	hypothetical prote	327	54	11.7	1283	2	T18939	hypothetical prote
255	54.5	11.8	282	2	PQ0376	cell fusion glycop	328	53.5	11.6	114	2	C90344	oleosin-like prote
256	54.5	11.8	296	2	F83145	probable epoxide h	329	53.5	11.6	153	2	T49895	hypothetical prote
257	54.5	11.8	296	2	A85698	transposase for IS	330	53.5	11.6	173	2	S01145	hypothetical prote
258	54.5	11.8	296	2	A99840	transposase for IS	331	53.5	11.6	211	2	G82573	CDP-diacylglycerol
259	54.5	11.8	304	2	S59965	phosphotransferase	332	53.5	11.6	225	1	CYRGE	epsilon-crystallin
260	54.5	11.8	337	2	G87487	conserved hypothet	333	53.5	11.6	269	2	D96957	uncharacterized me
261	54.5	11.8	362	2	S77244	biotin synthase [E	334	53.5	11.6	282	2	PQ0388	cell fusion glycop
262	54.5	11.8	369	2	E81722	hypothetical prote	335	53.5	11.6	296	2	C90978	IS629 transposase
263	54.5	11.8	373	2	G85355	nodulin-like prote	336	53.5	11.6	296	2	H85824	IS629 transposase
264	54.5	11.8	393	2	AB0035	cystathionine beta	337	53.5	11.6	303	2	T13598	trypsin homolog -
265	54.5	11.8	422	2	T07967	mandelonitrile lyase	338	53.5	11.6	307	2	B72922	conserved hypothet
266	54.5	11.8	445	1	S54140	D-serine permease	339	53.5	11.6	339	2	H71265	hypothetical prote
267	54.5	11.8	458	1	YTBSTR	tetracycline resis	340	53.5	11.6	346	2	D70558	probable cydB prot
268	54.5	11.8	458	1	YTSOG	tetracycline resis	341	53.5	11.6	357	2	F81679	chorismate synthas
269	54.5	11.8	458	1	YTB5U6	tetracycline resis	342	53.5	11.6	376	2	AF1943	multidrug-efflux t
270	54.5	11.8	458	2	JQ1211	tetracycline resis	343	53.5	11.6	378	2	T34372	hypothetical prote
271	54.5	11.8	458	2	S23743	tetracycline resis	344	53.5	11.6	383	2	T48018	hypothetical prote
272	54.5	11.8	483	1	A53595	tetracycline resis	345	53.5	11.6	410	2	A48585	transcription fact
273	54.5	11.8	484	2	T00158	allantoinase [EC 3	346	53.5	11.6	412	2	AH3274	macrolide-efflux p
274	54.5	11.8	501	2	E87239	amidase [EC 3.5.-	347	53.5	11.6	461	2	T06936	photosystem II chl
275	54.5	11.8	576	2	A49933	aldehyde dehydroge	348	53.5	11.6	495	2	I57680	potassium channel
276	54.5	11.8	586	2	T48672	proteinase SM tran	349	53.5	11.6	495	2	A40090	potassium channel
277	54.5	11.8	622	2	AC1236	ABC-type transport	350	53.5	11.6	495	2	B91113	potassium channel
278	54.5	11.8	628	2	T01467	acylttransferase (t	351	53.5	11.6	529	2	H84049	hypothetical prote
279	54.5	11.8	722	2	B71728	hypothetical prote	352	53.5	11.6	539	2	T32693	hypothetical prote
280	54.5	11.8	735	2	E69139	probable peptidase	353	53.5	11.6	546	2	S47300	gene F protein - r
281	54.5	11.8	895	2	I54343	hypothetical prote	354	53.5	11.6	553	1	VGNZMV	cell fusion glycop
282	54.5	11.8	895	2	S20582	dystroglycan - hum	355	53.5	11.6	556	2	T03114	tegument protein -
283	54.5	11.8	900	2	G87431	dystrophin-associa	356	53.5	11.6	571	1	H65169	probable transport
284	54.5	11.8	1044	2	T31072	pyruvate phosphate	357	53.5	11.6	571	2	D91206	probable cotranspo
285	54.5	11.8	1044	2	AB2158	heterocyst differe	358	53.5	11.6	571	2	F86052	probable cotranspo
286	54.5	11.8	1099	2	T14850	S-layer protein pr	359	53.5	11.6	594	2	T43246	amino acid transpo
287	54.5	11.8	1146	2	B35962	protein-tyrosine k	360	53.5	11.6	597	2	AH2351	probable secreted
288	54.5	11.8	1182	2	A35962	protein-tyrosine k	361	53.5	11.6	890	2	T35237	probable secreted
289	54	11.7	98	2	T17183	NADH2 dehydrogenas	362	53.5	11.6	945	2	S30398	aminopeptidase N h
290	54	11.7	98	2	T17348	NADH2 dehydrogenas	363	53.5	11.6	985	2	T10339	DNA-directed DNA p
291	54	11.7	154	1	MMBE16	16.9k membrane pro	364	53.5	11.6	1045	2	E90705	hypothetical prote
292	54	11.7	168	2	S47881	NADH2 dehydrogenas	365	53.5	11.6	1045	2	H85555	hypothetical prote
293	54	11.7	188	2	A75382	hypothetical prote	366	53.5	11.6	1047	2	E64790	YbdE protein - Esc
294	54	11.7	248	1	PRMSC2	granzyme C [EC 3.4	367	53.5	11.6	1075	2	S76433	cation efflux sysc
295	54	11.7	259	2	C64481	conserved hypothet	368	53.5	11.6	1175	2	S51005	protein-tyrosine-p
296	54	11.7	292	2	T14627	hypothetical prote	369	53.5	11.6	2037	1	T16881	hypothetical prote
297	54	11.7	316	2	F91044	transaldolase A [i	370	53.5	11.6	3566	1	A40701	tenascin-X precurs
298	54	11.7	316	2	A85889	transaldolase A [i	371	53	11.5	90	2	T33692	hypothetical prote
299	54	11.7	316	2	G65021	transaldolase [EC	372	53	11.5	148	2	A84636	similar to avrRpt2
300	54	11.7	328	2	A69218	hypothetical prote	373	53	11.5	154	1	F70002	conserved hypothet
301	54	11.7	346	2	A69218	cysteine proteinas	374	53	11.5	166	2	D58889	NADH2 dehydrogenas
302	54	11.7	346	2	C86413	rod outer segment	375	53	11.5	201	2	A71124	hypothetical prote
303	54	11.7	356	2	I68620	cysteine proteinas	376	53	11.5	202	2	JC6205	cell surface antig
304	54	11.7	356	2	S66348	hypothetical prote	377	53	11.5	210	2	JC5448	serine proteinase
305	54	11.7	359	2	F69061	hypothetical prote	378	53	11.5	214	2	AH0265	probable membrane
306	54	11.7	386	2	A72313	hypothetical prote	379	53	11.5	216	2	JC7930	small neutral amin
307	54	11.7	394	2	C64185	cell division prot	380	53	11.5	224	2	S67949	beta-tubulin ASL1
308	54	11.7	428	2	S08084	gene IV protein -	381	53	11.5	224	2	S73823	MG243 homolog H91
309	54	11.7	440	2	E84118	UDP-N-acetylglucos	382	53	11.5	257	2	D71544	hypothetical prote
310	54	11.7	456	2	AH0551	proline-specific p	383	53	11.5	264	2	A75076	membrane protein p
311	54	11.7	476	2	T40086	hypothetical prote	384	53	11.5	279	2	A95933	probable inositol
312	54	11.7	549	2	C86692	peptide-binding pr	385	53	11.5	300	2	B83100	inhibitor of chrom
313	54	11.7	558	2	AE1236	glycerol 3 phospho	386	53	11.5	306	2	A88040	protein F47F6.1 [i
314	54	11.7	573	1	S33212	INDAI protein - fu	387	53	11.5	310	2	D87704	integral membrane
315	54	11.7	604	2	B84221	hypothetical prote	388	53	11.5	339	2	AG0165	L-allo-threonine a
316	54	11.7	625	2	T25373	hypothetical prote	389	53	11.5	342	2	A44965	cysteine proteinas
317	54	11.7	634	2	T33528	hypothetical prote	390	53	11.5	342	2	A45524	cysteine proteinas
318	54	11.7	787	2	T38224	probable glycosyl	391	53	11.5	364	2	AH1857	anthranilate phosph
319	54	11.7	869	2	A96558	probable protein k	392	53	11.5	376	2	E95879	probable sugar ABC
320	54	11.7	880	2	S49627	regulatory protein	393	53	11.5	377	2	A53044	geranylgeranyl-dip
321	54	11.7	885	2	G83260	aminopeptidase N p	394	53	11.5	385	2	A91178	probable membrane

103	58	12.6	185	2	AG1054	probable exported	176	56	12.1	594	2	A83096	probable permease
104	58	12.6	196	2	E75612	hypothetical prote	177	56	12.1	626	2	D70178	PTS system, fructo
105	58	12.6	215	2	AF0650	probable membrane	178	56	12.1	736	2	C69451	cationic amino aci
106	58	12.6	257	2	A64459	diphthine synthase	179	56	12.1	1118	2	C95385	probable adenylate
107	58	12.6	277	2	S44252	raffinose operon r	180	56	12.1	1305	2	AB0168	probable cell divi
108	58	12.6	368	2	T26425	hypothetical prote	181	56	12.1	2055	2	T30259	multiple PDZ domai
109	58	12.6	376	2	AH1795	hypothetical membr	182	56	12.1	3329	2	T42205	breast cancer susc
110	58	12.6	398	2	A82081	cell division prot	183	56	12.1	5170	2	T15348	hypothetical prote
111	58	12.6	462	2	F75888	probable kynurenin	184	55.5	12.0	245	2	A90527	hypothetical prote
112	58	12.6	4836	2	T14346	hcr2 protein - mo	185	55.5	12.0	249	4	T44821	bacteriorhodopsin
113	57.5	12.5	71	2	D23876	vitellogenin B2 pr	186	55.5	12.0	254	2	F75496	conserved hypotet
114	57.5	12.5	139	2	AF06805	hypothetical prote	187	55.5	12.0	256	2	E75401	hypothetical prote
115	57.5	12.5	324	2	T36805	conserved hypotet	188	55.5	12.0	259	4	T44820	bacteriorhodopsin
116	57.5	12.5	342	2	A47673	photosystem II chl	189	55.5	12.0	262	1	RAHSB	bacteriorhodopsin
117	57.5	12.5	356	2	C72475	hypothetical prote	190	55.5	12.0	262	2	H84300	bacteriorhodopsin
118	57.5	12.5	374	2	T10415	virus envelope pro	191	55.5	12.0	270	2	B29934	pancreatic elastas
119	57.5	12.5	461	2	B83601	probable transport	192	55.5	12.0	299	2	B83243	hypothetical prote
120	57.5	12.5	461	2	AF05079	C4-dicarboxylate a	193	55.5	12.0	309	2	C95138	tagatose-6-phospha
121	57.5	12.5	523	2	B83629	probable ATP-bindi	194	55.5	12.0	309	2	A98006	tagatose-6-phospha
122	57.5	12.5	528	2	I84205	potassium channel	195	55.5	12.0	316	2	G75388	hypothetical prote
123	57.5	12.5	594	2	B90586	transport protein	196	55.5	12.0	317	2	S16299	exoz protein - Rhi
124	57.5	12.5	636	2	S47299	gene F protein - r	197	55.5	12.0	317	2	B95975	acetyltransferase
125	57.5	12.5	662	2	T44219	hypothetical prote	198	55.5	12.0	344	2	S42648	photosystem II chl
126	57.5	12.5	662	2	T44034	hypothetical prote	199	55.5	12.0	344	2	AB2306	photosystem II chl
127	57.5	12.5	1902	1	B44858	lactocepin (EC 3.4	200	55.5	12.0	346	2	C71042	probable threonine
128	57	12.4	148	2	C84690	probable membrane	201	55.5	12.0	376	2	F72868	occlusion-derived
129	57	12.4	185	2	JN0766	adrenomedullin pre	202	55.5	12.0	383	2	S53379	probable membrane
130	57	12.4	258	2	F71251	probable uridine p	203	55.5	12.0	385	2	F86464	hypothetical prote
131	57	12.4	269	2	AG2268	hypothetical prote	204	55.5	12.0	389	2	B81347	probable aspartate
132	57	12.4	342	2	A30189	iron stress-induce	205	55.5	12.0	456	2	T22347	hypothetical prote
133	57	12.4	374	2	T05660	hypothetical prote	206	55.5	12.0	459	2	D86669	amino acid permeas
134	57	12.4	374	2	T00561	nodulin-like prote	207	55.5	12.0	545	2	A12327	hypothetical prote
135	57	12.4	385	2	T04725	hypothetical prote	208	55.5	12.0	609	2	S28283	hypothetical prote
136	57	12.4	440	2	H86312	F2H15.2 protein -	209	55.5	12.0	625	2	S13919	potassium channel
137	57	12.4	456	2	B96902	membrane protein,	210	55.5	12.0	648	2	C71658	probable pinosoma
138	57	12.4	457	2	B64769	proline transport	211	55.5	12.0	716	2	T03695	delta 1 pyrroline-
139	57	12.4	457	2	D90685	proline permease t	212	55.5	12.0	851	2	T12503	hypothetical prote
140	57	12.4	457	2	H85535	proline permease t	213	55.5	12.0	946	1	A29550	methylene-tetrahydr
141	57	12.4	461	2	D90711	C4-dicarboxylate a	214	55.5	12.0	1217	2	T22672	hypothetical prote
142	57	12.4	461	2	C64796	dcuC protein - Esc	215	55.5	12.0	1423	2	A49206	exo-beta-D-fructos
143	57	12.4	461	2	H85561	transport of dicar	216	55.5	12.0	2054	2	T46612	multi PDZ domain p
144	57	12.4	487	2	S73277	photosystem II 44K	217	55	11.9	52	2	T32956	hypothetical prote
145	56.5	12.3	114	2	E43559	homeotic protein R	218	55	11.9	52	2	T33694	hypothetical prote
146	56.5	12.3	187	2	S70186	21K protein - Shig	219	55	11.9	128	2	F71371	hypothetical prote
147	56.5	12.3	191	2	AD0905	probable exported	220	55	11.9	169	2	S18653	hypothetical prote
148	56.5	12.3	233	2	F70668	probable lipoprote	221	55	11.9	212	2	S82125	conserved hypotet
149	56.5	12.3	258	2	D84336	uridine phosphoryl	222	55	11.9	268	2	S05471	embryonic abundan
150	56.5	12.3	361	2	S19552	potassium channel	223	55	11.9	268	2	S14068	seed protein precu
151	56.5	12.3	419	2	S22136	endothiapepsin (EC	224	55	11.9	288	2	T12462	hypothetical prote
152	56.5	12.3	471	2	T04911	hypothetical prote	225	55	11.9	312	2	B75405	endopeptidase-rela
153	56.5	12.3	485	2	E97506	potassium uptake p	226	55	11.9	334	2	S54438	hemin permease [va
154	56.5	12.3	500	2	F97025	spoVB related memb	227	55	11.9	336	2	AH0201	probable zinc-bind
155	56.5	12.3	614	2	A69845	Na+/H+ antiporter	228	55	11.9	340	2	AF2896	hypothetical prote
156	56.5	12.3	670	1	E70040	conserved hypotet	229	55	11.9	340	2	H97671	hypothetical prote
157	56.5	12.3	686	1	VGBENA	glycoprotein H pre	230	55	11.9	344	2	E84043	glycerolaldehyde-3-p
158	56.5	12.3	686	2	S15478	glycoprotein H pre	231	55	11.9	357	2	A23641	RP2 protein, test
159	56.5	12.3	886	2	S25359	hypothetical prote	232	55	11.9	376	1	S17246	chorismate synthas
160	56.5	12.3	852	2	T1EPVK	K+ channel blocker	233	55	11.9	404	2	S34031	Ktr3 protein - yea
161	56	12.1	79	1	T1EPVK	hypothetical prote	234	55	11.9	410	2	AH2895	hypothetical prote
162	56	12.1	196	2	F64231	hypothetical prote	235	55	11.9	410	2	C97671	probable maltose-b
163	56	12.1	222	2	F82353	conserved hypotet	236	55	11.9	443	2	B86180	protein TIG11.3 li
164	56	12.1	261	2	AB2966	conserved hypotet	237	55	11.9	459	2	A87201	conserved hypotet
165	56	12.1	261	2	B98317	ATP synthase chain	238	55	11.9	461	2	S57713	probable mannosyl
166	56	12.1	388	2	T09885	hypothetical prote	239	55	11.9	473	1	F2KK4C	photosystem II chl
167	56	12.1	411	2	C87586	metal ion efflux m	240	55	11.9	482	2	AG1147	P60 extracellular
168	56	12.1	436	2	G70058	hypothetical prote	241	55	11.9	484	2	A41487	protein P60 precu
169	56	12.1	440	2	C97376	probable transport	242	55	11.9	654	2	A96235	hydroxamate-depend
170	56	12.1	440	2	A12593	MFS permease limpo	243	55	11.9	654	2	AC3051	hypothetical prote
171	56	12.1	449	2	H70546	hypothetical prote	244	55	11.9	716	2	E69672	penicillin-binding
172	56	12.1	503	2	S36514	Li protein - human	245	55	11.9	2531	2	S18188	notch-1 protein homo
173	56	12.1	547	2	D95337	probable manganese	246	55	11.9	2531	2	A46019	translocon-associa
174	56	12.1	558	2	S29125	dimethylalanine mo	247	54.5	11.8	173	2	S33295	hypothetical prote
175	56	12.1	578	2	B37852	phosphotransferase	248	54.5	11.8	177	2	G75285	hypothetical prote

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OM protein - protein search, using sw model

Run on: November 21, 2006, 19:45:28 ; Search time 41 Seconds  
(without alignments)  
208.861 Million cell updates/sec

Title: US-10-063-557-50  
Perfect score: 461  
Sequence: 1 MERVIALLLAGLTALEN.....HSPVPEKAIPITPGSATTC 89

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : PIR 80:\*

1: Pir1:\*

2: Pir2:\*

3: Pir3:\*

4: Pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	256.5	55.6	87	2 I59391	transmembrane prot
2	241.5	52.4	88	2 S61552	mammary tumor prot
3	214.5	46.5	87	2 A55571	chloride conductan
4	126.5	27.4	92	2 A40533	CAMP-dependent pro
5	96.5	20.9	58	2 D46435	Na+/K+-exchanging
6	94.5	20.5	53	2 A46435	Na+/K+-exchanging
7	75.5	16.4	58	2 B46435	Na+/K+-exchanging
8	73.5	15.9	58	2 C46435	Na+/K+-exchanging
9	72	15.6	160	1 A61088	plastoquinol-plast
10	71	15.4	529	2 F69989	conserved hypotet
11	69	15.0	150	2 A80371	probable membrane
12	67.5	14.6	135	2 A05009	hypothetical prote
13	66.5	14.4	359	2 B86620	chorismate synthas
14	66.5	14.4	359	2 A72004	chorismate synthas
15	66.5	14.4	523	2 A38101	potassium channel
16	66	14.3	446	2 B90463	proline/betaine tr
17	64	13.9	525	2 A43531	potassium channel
18	63.5	13.8	309	2 AC1697	probable transport
19	63.5	13.8	309	2 A11325	probable transport
20	63.5	13.8	511	2 A46020	potassium channel
21	63.5	13.8	511	2 S07095	potassium channel
22	63.5	13.8	585	2 A39395	delayed rectifier
23	63.5	13.8	620	2 A70525	hypothetical prote
24	63	13.7	468	2 C96818	hypothetical prote
25	62.5	13.6	299	2 A38111	transcription regu
26	62.5	13.6	679	2 A42073	potassium channel
27	62.5	13.6	769	2 I56546	Shaw type potassi
28	62.5	13.6	910	2 F81974	leucine-tRNA ligas
29	62	13.4	381	2 AB2907	GGDEF family prote

30	62	13.4	393	2 B97682	ggdef family prote
31	62	13.4	589	2 U43295	uracil transport p
32	62	13.4	777	2 S30271	pyocin AP41 large
33	61.5	13.3	342	2 S75086	iron-stress chloro
34	61.5	13.3	433	2 B72025	flagellum-specific
35	61.5	13.3	433	2 A81513	virulence Atfase,
36	61.5	13.3	433	2 H86597	flagellum-specific
37	61.5	13.3	445	2 AD0962	DsdX permease (imp
38	61.5	13.3	990	2 JC8058	laeverin - human
39	61.5	13.3	1499	2 AC2555	hypothetical prote
40	61	13.2	268	2 C87295	conserved hypotet
41	61	13.2	355	2 I51157	major histocompati
42	61	13.2	461	2 B90984	O antigen flippase
43	61	13.2	463	2 A75151	damage-inducible p
44	61	13.2	463	2 E85829	O antigen flippase
45	61	13.2	463	2 G71191	probable DNA damag
46	61	13.2	520	2 D84471	probable membrane
47	60.5	13.1	295	2 C84830	probable protein k
48	60.5	13.1	312	2 B83749	sugar transport sy
49	60.5	13.1	326	2 C90272	hypothetical prote
50	60.5	13.1	354	2 G86276	hypothetical prote
51	60.5	13.1	427	2 E87669	conserved hypotet
52	60.5	13.1	463	2 A10388	probable proline-s
53	60.5	13.1	516	2 T47509	potassium channel
54	60.5	13.1	581	2 S17150	potassium channel
55	60.5	13.1	613	2 A39402	potassium channel
56	60.5	13.1	624	2 S22703	voltage-gated pota
57	60.5	13.1	728	2 B81370	phosphoribosylform
58	60	13.0	71	2 C23876	vitellinogen B1 pr
59	60	13.0	208	2 S36155	paired box protein
60	60	13.0	269	2 AH1970	type 4 prepilin pe
61	60	13.0	342	2 S77652	transcription fact
62	60	13.0	412	2 A83461	hypothetical prote
63	60	13.0	497	1 WBEELM	membrane protein L
64	60	13.0	538	2 A65175	hypothetical 60.6
65	60	13.0	5232	2 A45086	HC-toxin synthetas
66	59.5	12.9	267	2 G86782	phosphomethylpyrim
67	59.5	12.9	298	2 A82387	amino acid ABC tra
68	59.5	12.9	356	2 T30361	occlusion-derived
69	59.5	12.9	527	2 A48076	glucose transporte
70	59.5	12.9	527	2 A45611	probable hexose tr
71	59	12.8	130	2 B85808	unknown protein en
72	59	12.8	175	2 T11087	NADH2 dehydrogenas
73	59	12.8	177	2 AH1669	probable NAD(p)H o
74	59	12.8	215	2 E85704	probable channel p
75	59	12.8	215	2 F90846	probable channel p
76	59	12.8	215	2 E64871	probable membrane
77	59	12.8	310	2 G87624	integral membrane
78	59	12.8	326	2 AB3607	3-oxoacyl-[acyl-ca
79	59	12.8	419	2 E90446	permease (imported
80	59	12.8	420	2 G96002	probable sugar upt
81	59	12.8	479	2 C95366	NADH2 dehydrogenas
82	59	12.8	558	2 A39322	glycerol 3 phospho
83	59	12.8	653	2 A39922	potassium channel
84	59	12.8	654	2 S11049	potassium channel
85	59	12.8	660	2 S24125	potassium channel
86	59	12.8	802	2 JH0595	potassium channel
87	59	12.8	853	1 CHKD1	potassium channel
88	59	12.8	857	2 I56529	potassium channel
89	59	12.8	858	2 S31761	potassium channel
90	58.5	12.7	182	2 C83600	hypothetical prote
91	58.5	12.7	384	2 A12962	cellulose synthesi
92	58.5	12.7	389	2 E98320	hypothetical prote
93	58.5	12.7	411	2 H75376	hypothetical prote
94	58.5	12.7	425	2 T50355	hypothetical prote
95	58.5	12.7	463	2 D87201	conserved hypotet
96	58.5	12.7	633	2 E86271	protein F16A14.4 [
97	58.5	12.7	876	2 G81029	leucine-tRNA ligas
98	58.5	12.7	1095	2 E96744	probable oligopept
99	58.5	12.7	1189	2 I39711	celE protein - Agr
100	58.5	12.7	2712	2 T30949	hypothetical prote
101	58.5	12.7	3864	2 D87757	protein C44E4.1a [
102	58	12.6	114	2 F69782	hypothetical prote

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993	50	10.8	1703	7	US-11-455-703-8	Sequence 8, Appl	1086	49.5	10.7	428	6	US-10-612-783-4764	Sequence 4764, Ap
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742	51	11.1	346	7	US-11-056-355B-38554	Sequence 38554, A	815	51	11.1	2625	6	US-10-526-572-34	Sequence 34, Appl
743	51	11.1	354	7	US-11-056-355B-55079	Sequence 55079, A	816	51	11.1	3664	6	US-10-574-398-79	Sequence 79, Appl
744	51	11.1	366	7	US-11-056-355B-38553	Sequence 38553, A	817	51	11.1	4834	6	US-10-505-928-827	Sequence 827, App
745	51	11.1	379	7	US-11-330-403-11043	Sequence 11043, A	818	50.5	11.0	86	6	US-10-449-902-38839	Sequence 38839, A
746	51	11.1	382	6	US-10-449-902-52918	Sequence 52918, A	819	50.5	11.0	87	6	US-10-805-394-4015	Sequence 4015, Ap
747	51	11.1	383	7	US-11-056-355B-52712	Sequence 52712, A	820	50.5	11.0	139	6	US-10-953-349-12302	Sequence 12302, A
748	51	11.1	384	7	US-11-058-746-7	Sequence 7, Appl	821	50.5	11.0	152	6	US-10-953-349-12301	Sequence 12301, A
749	51	11.1	389	7	US-11-056-355B-38552	Sequence 38552, A	822	50.5	11.0	155	7	US-11-107-336-65	Sequence 65, Appl
750	51	11.1	389	7	US-11-330-403-16054	Sequence 16054, A	823	50.5	11.0	189	6	US-10-953-349-12300	Sequence 12300, A
751	51	11.1	399	7	US-11-330-403-17090	Sequence 17090, A	824	50.5	11.0	249	6	US-10-805-394-6183	Sequence 6183, Ap
752	51	11.1	402	6	US-10-953-349-31320	Sequence 31320, A	825	50.5	11.0	250	7	US-11-330-403-16890	Sequence 16890, A
753	51	11.1	402	6	US-10-449-902-48763	Sequence 48763, A	826	50.5	11.0	275	6	US-10-805-394-4187	Sequence 4187, Ap
754	51	11.1	410	6	US-10-953-349-31319	Sequence 31319, A	827	50.5	11.0	294	6	US-10-449-902-30124	Sequence 30124, A
755	51	11.1	421	7	US-11-330-403-2284	Sequence 2284, Ap	828	50.5	11.0	295	6	US-10-449-902-48737	Sequence 48737, A
756	51	11.1	444	6	US-10-953-349-31318	Sequence 31318, A	829	50.5	11.0	303	7	US-11-056-355B-102098	Sequence 102098, A
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762	51	11.1	536	6	US-10-805-394-6061	Sequence 6061, Ap	835	50.5	11.0	330	7	US-11-434-137-6080	Sequence 6080, Ap
763	51	11.1	546	7	US-11-056-355B-44093	Sequence 44093, A	836	50.5	11.0	330	7	US-11-434-184-6080	Sequence 6080, Ap
764	51	11.1	546	7	US-11-056-355B-73985	Sequence 73985, A	837	50.5	11.0	330	7	US-11-434-199-6080	Sequence 6080, Ap
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547	52	11.3	162	6	US-10-449-902-41668	Sequence 41668, A	626	51.5	11.2	327	7	US-11-056-355B-55937	Sequence 55937, A
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551	52	11.3	207	7	US-11-056-355B-74387	Sequence 74387, A	630	51.5	11.2	344	7	US-11-434-199-3460	Sequence 3460, Ap
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556	52	11.3	250	6	US-10-449-902-51855	Sequence 51855, A	635	51.5	11.2	373	7	US-11-056-355B-55935	Sequence 55935, A
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558	52	11.3	297	6	US-11-295-040-10	Sequence 10, Appl	637	51.5	11.2	378	6	US-10-669-920-490	Sequence 490, App
559	52	11.3	297	6	US-10-374-780A-2898	Sequence 2898, Ap	638	51.5	11.2	378	6	US-10-669-920-493	Sequence 493, App
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572	52	11.3	360	6	US-11-056-355B-63741	Sequence 63741, A	651	51.5	11.2	474	7	US-11-090-997-300	Sequence 300, App
573	52	11.3	375	6	US-10-953-349-29193	Sequence 29193, A	652	51.5	11.2	474	7	US-11-361-871-24	Sequence 24, Appl
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580	52	11.3	470	6	US-10-953-349-21134	Sequence 21134, A	659	51.5	11.2	537	6	US-10-486-306-13	Sequence 13, Appl
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586	52	11.3	581	7	US-11-330-403-916	Sequence 916, App	665	51.5	11.2	616	6	US-10-526-324-1280	Sequence 1280, Ap
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595	52	11.3	2057	7	US-11-011-702-30	Sequence 30, Appl	674	51.5	11.2	889	6	US-10-449-902-55493	Sequence 55493, A
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599	52	11.3	2169	7	US-11-051-725-5	Sequence 5, Appl	678	51.5	11.2	2303	7	US-11-335-891-32	Sequence 32, Appl
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399	53.5	11.6	271	7	US-11-434-184-7984	Sequence 7984, Ap	472	53	11.5	637	6	US-10-953-349-7922	Sequence 7922, Ap
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412	53.5	11.6	384	6	US-10-526-324-1723	Sequence 1723, Ap	485	53	11.5	702	7	US-11-056-355B-39889	Sequence 39889, A
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415	53.5	11.6	405	6	US-10-449-902-36521	Sequence 36521, A	488	53	11.5	1070	6	US-10-570-909-80	Sequence 80, Appl
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418	53.5	11.6	485	7	US-11-056-355B-86768	Sequence 86768, A	491	53	11.5	1146	6	US-10-620-061-9	Sequence 9, Appl
419	53.5	11.6	485	7	US-11-056-355B-86768	Sequence 86768, A	492	53	11.5	1324	6	US-10-833-833-40	Sequence 40, Appl
420	53.5	11.6	495	7	US-11-313-450-19	Sequence 19, Appl	493	53	11.5	1463	6	US-10-833-833-36	Sequence 36, Appl
421	53.5	11.6	504	7	US-11-056-355B-73783	Sequence 73783, A	494	53	11.5	1463	6	US-10-833-833-36	Sequence 36, Appl
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430	53	11.5	219	6	US-10-805-394-5067	Sequence 5067, Ap	503	53	11.5	285	7	US-11-330-403-16657	Sequence 16657, A
431	53	11.5	232	6	US-10-449-902-32304	Sequence 32304, A	504	53	11.5	292	7	US-11-056-355B-9533	Sequence 9533, Ap
432	53	11.5	237	7	US-11-319-952-66	Sequence 66, Appl	505	53	11.5	292	7	US-11-056-355B-11156	Sequence 11156, A
433	53	11.5	243	7	US-11-366-486-941	Sequence 941, Appl	506	53	11.5	321	7	US-11-056-355B-9532	Sequence 9532, Ap
434	53	11.5	251	6	US-10-529-163-5	Sequence 5, Appl	507	53	11.5	321	7	US-11-056-355B-11155	Sequence 11155, A
435	53	11.5	251	7	US-11-319-952-67	Sequence 67, Appl	508	53	11.5	321	7	US-11-056-355B-11206	Sequence 11206, A
436	53	11.5	256	7	US-10-430-403-2298	Sequence 2298, Ap	509	53	11.5	324	6	US-10-545-100-9	Sequence 9, Appl
437	53	11.5	260	6	US-10-449-902-52480	Sequence 52480, A	510	53	11.5	342	6	US-10-612-783-6487	Sequence 6487, Ap
438	53	11.5	305	6	US-10-652-846-75	Sequence 75, Appl	511	53	11.5	354	7	US-11-056-355B-9531	Sequence 9531, Ap
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443	53	11.5	356	7	US-11-056-355B-95047	Sequence 95047, A	516	53	11.5	357	7	US-11-056-355B-11184	Sequence 11184, A
444	53	11.5	357	7	US-11-330-403-13715	Sequence 13715, A	517	53	11.5	369	6	US-10-805-394-5658	Sequence 5658, Ap
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446	53	11.5	357	7	US-11-056-355B-95046	Sequence 95046, A	519	53	11.5	374	6	US-10-449-902-32419	Sequence 32419, A
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449	53	11.5	362	7	US-11-056-355B-16023	Sequence 16023, A	522	53	11.5	458	6	US-10-449-902-56530	Sequence 56530, A
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453	53	11.5	399	7	US-11-056-355B-94621	Sequence 94621, A	526	53	11.5	502	7	US-11-056-355B-116440	Sequence 116440, A
454	53	11.5	421	7	US-11-330-403-15378	Sequence 15378, A	527	53	11.5	507	6	US-10-449-902-47135	Sequence 47135, A
455	53	11.5	421	7	US-11-330-403-11121	Sequence 11121, A	528	53	11.5	551	7	US-11-236-238-29	Sequence 29, Appl
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457	53	11.5	443	7	US-11-056-355B-79230	Sequence 79230, A	530	53	11.5	583	6	US-10-449-902-48162	Sequence 48162, A
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461	53	11.5	548	7	US-11-056-355B-70616	Sequence 70616, A	534	53	11.5	612	7	US-11-056-355B-40740	Sequence 40740, A
462	53	11.5	548	7	US-11-056-355B-80747	Sequence 80747, A	535	53	11.5	616	7	US-11-056-355B-105199	Sequence 105199, A
463	53	11.5	554	7	US-11-056-355B-90864	Sequence 90864, A	536	53	11.5	616	7	US-11-056-355B-116438	Sequence 116438, A
464	53	11.5	554	7	US-11-056-355B-94620	Sequence 94620, A	537	53	11.5	673	6	US-10-449-902-54937	Sequence 54937, A
465	53	11.5	577	6	US-10-953-349-7923	Sequence 7923, Ap	538	53	11.5	763	7	US-11-311-454-88	Sequence 88, Appl
466	53	11.5	577	7	US-11-056-355B-39891	Sequence 39891, A	539	53	11.5	800	6	US-10-449-902-34842	Sequence 34842, A
467	53	11.5	577	7	US-11-056-355B-70615	Sequence 70615, A	540	53	11.5	1000	6	US-10-743-891A-25	Sequence 25, Appl
468	53	11.5	577	7	US-11-056-355B-84485	Sequence 84485, A	541	53	11.5	1005	7	US-11-311-454-2	Sequence 2, Appl
469	53	11.5	603	7	US-11-056-355B-70555	Sequence 70555, A	542	53	11.5	1373	7	US-11-311-454-1	Sequence 1, Appl
470	53	11.5	607	7	US-11-056-355B-78200	Sequence 78200, A	543	53	11.5	2000	7	US-11-311-454-82	Sequence 82, Appl



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254	55	11.9	152	7	US-11-056-355B-113903	Sequence 113903, A	327	54	11.7	139	7	US-11-056-355B-15263	Sequence 15263, A
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256	55	11.9	159	7	US-11-434-184-1062	Sequence 1062, Ap	329	54	11.7	194	7	US-11-056-355B-11187	Sequence 11187, A
257	55	11.9	159	7	US-11-434-199-1062	Sequence 1062, Ap	330	54	11.7	237	7	US-11-056-355B-10516	Sequence 10516, A
258	55	11.9	159	7	US-11-434-203-1062	Sequence 1062, Ap	331	54	11.7	237	7	US-11-056-355B-11186	Sequence 11186, A
259	55	11.9	185	7	US-11-056-355B-38484	Sequence 38484, A	332	54	11.7	246	7	US-11-056-355B-15262	Sequence 15262, A
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273	55	11.9	410	6	US-10-953-349-23326	Sequence 23326, A	346	54	11.7	304	7	US-11-056-355B-83069	Sequence 83069, A
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283	54.5	11.8	158	7	US-11-056-355B-115990	Sequence 115990, A	356	54	11.7	346	7	US-11-056-355B-83067	Sequence 83067, A
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285	54.5	11.8	165	7	US-11-056-355B-115989	Sequence 115989, A	358	54	11.7	355	6	US-10-953-349-31241	Sequence 31241, A
286	54.5	11.8	185	6	US-10-374-780A-106	Sequence 106, App	359	54	11.7	355	6	US-10-526-324-2125	Sequence 2125, Ap
287	54.5	11.8	185	7	US-11-056-355B-22151	Sequence 22151, A	360	54	11.7	357	7	US-11-056-355B-65700	Sequence 65700, A
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295	54.5	11.8	276	6	US-10-353-349-15535	Sequence 15535, A	368	54	11.7	404	7	US-11-330-403-17492	Sequence 17492, A
296	54.5	11.8	280	6	US-10-449-902-41443	Sequence 41443, A	369	54	11.7	421	7	US-11-366-486-939	Sequence 939, App
297	54.5	11.8	283	6	US-11-330-403-10306	Sequence 10306, A	370	54	11.7	451	7	US-11-056-355B-59741	Sequence 59741, A
298	54.5	11.8	293	6	US-10-953-349-38938	Sequence 38938, A	371	54	11.7	470	7	US-11-366-486-673	Sequence 673, App
299	54.5	11.8	294	7	US-11-056-355B-47598	Sequence 47598, A	372	54	11.7	520	7	US-11-056-355B-59740	Sequence 59740, A
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303	54.5	11.8	340	7	US-11-056-355B-47596	Sequence 47596, A	376	53.5	11.6	118	7	US-11-056-355B-28734	Sequence 28734, A
304	54.5	11.8	358	6	US-10-449-902-30910	Sequence 30910, A	377	53.5	11.6	118	7	US-11-056-355B-28733	Sequence 28733, A
305	54.5	11.8	382	6	US-10-449-902-39662	Sequence 39662, A	378	53.5	11.6	122	7	US-11-056-355B-112291	Sequence 112291, A
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307	54.5	11.8	384	7	US-11-340-318-4	Sequence 4, Appli	380	53.5	11.6	149	7	US-11-056-355B-101051	Sequence 101051, A
308	54.5	11.8	394	6	US-10-953-349-38936	Sequence 38936, A	381	53.5	11.6	153	7	US-11-056-355B-112290	Sequence 112290, A
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310	54.5	11.8	445	7	US-11-289-989-15	Sequence 15, Appli	383	53.5	11.6	159	7	US-11-056-355B-28732	Sequence 28732, A
311	54.5	11.8	478	6	US-10-449-902-47028	Sequence 47028, A	384	53.5	11.6	159	7	US-11-056-355B-32322	Sequence 32322, A
312	54.5	11.8	481	7	US-11-249-111-77	Sequence 77, Appli	385	53.5	11.6	162	7	US-11-330-403-3442	Sequence 3442, Ap
313	54.5	11.8	509	6	US-10-449-902-47261	Sequence 47261, A	386	53.5	11.6	163	7	US-11-056-355B-101050	Sequence 101050, A
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316	54.5	11.8	815	6	US-10-449-902-52285	Sequence 52285, A	389	53.5	11.6	221	7	US-11-056-355B-5083	Sequence 5083, Ap
317	54.5	11.8	859	6	US-10-449-902-43366	Sequence 43366, A	390	53.5	11.6	221	7	US-11-330-403-369	Sequence 369, App
318	54.5	11.8	1146	7	US-11-274-081-3	Sequence 3, Appli	391	53.5	11.6	221	7	US-11-330-403-369	Sequence 369, App
319	54.5	11.8	1146	7	US-11-191-644-4	Sequence 4, Appli	392	53.5	11.6	239	7	US-11-319-952-71	Sequence 71, Appli
320	54.5	11.8	1182	7	US-11-191-644-5	Sequence 5, Appli	393	53.5	11.6	244	6	US-10-544-944-6	Sequence 6, Appli
321	54.5	11.8	1251	6	US-10-449-902-49449	Sequence 49449, A	394	53.5	11.6	244	6	US-10-546-435-4	Sequence 11, Appli
322	54.5	11.8	1385	7	US-11-191-644-20	Sequence 20, Appl	395	53.5	11.6	244	6	US-10-652-846-11	Sequence 11, Appli
323	54.5	11.8	1406	7	US-11-191-644-18	Sequence 18, Appl	396	53.5	11.6	244	7	US-11-319-952-84	Sequence 84, Appl
324	54	11.7	55	7	US-11-366-486-742	Sequence 742, App	397	53.5	11.6	259	7	US-11-330-403-6661	Sequence 6661, Ap



106	58.5	12.7	320	7	US-11-056-355B-117774	Sequence 117774,	179	57	12.4	184	7	US-11-056-355B-103216	Sequence 103216,
107	58.5	12.7	321	7	US-11-056-355B-46714	Sequence 26714, A	180	57	12.4	184	7	US-11-056-355B-114455	Sequence 114455,
108	58.5	12.7	350	7	US-11-056-355B-36367	Sequence 36367, A	181	57	12.4	210	7	US-11-056-355B-35886	Sequence 35886, A
109	58.5	12.7	356	7	US-11-056-355B-36366	Sequence 36366, A	182	57	12.4	210	7	US-11-056-355B-74435	Sequence 74435, A
110	58.5	12.7	377	7	US-11-056-355B-28876	Sequence 28876, A	183	57	12.4	229	6	US-11-049-902-39832	Sequence 39832, A
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112	58.5	12.7	377	7	US-11-056-355B-39929	Sequence 39929, A	185	57	12.4	233	7	US-11-330-403-14552	Sequence 14552, A
113	58.5	12.7	377	7	US-11-056-355B-42537	Sequence 42537, A	186	57	12.4	233	7	US-11-056-355B-20732	Sequence 20732, A
114	58.5	12.7	377	7	US-11-056-355B-75575	Sequence 75575, A	187	57	12.4	242	7	US-11-056-355B-77238	Sequence 77238, A
115	58.5	12.7	377	7	US-11-056-355B-98547	Sequence 98547, A	188	57	12.4	242	7	US-11-056-355B-7055	Sequence 7055, Ap
116	58.5	12.7	377	7	US-11-056-355B-109786	Sequence 109786,	189	57	12.4	253	6	US-10-953-349-7055	Sequence 7055, Ap
117	58.5	12.7	383	7	US-11-056-746-6	Sequence 6, Appl	190	57	12.4	253	7	US-11-056-355B-20731	Sequence 20731, A
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119	58.5	12.7	383	7	US-11-056-355B-32465	Sequence 32465, A	192	57	12.4	260	7	US-11-056-355B-74211	Sequence 74211, A
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11	94	20.4	178	7 US-11-090-997-1144	Sequence 1144, Ap
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761	214.5	46.5	87	4	US-10-295-027-1358
762	214.5	46.5	87	5	US-10-821-234-1279
763	214.5	46.5	87	5	US-10-475-075-192
764	214.5	46.5	87	5	US-10-475-075-192
765	214.5	46.5	87	6	US-11-051-454-140
766	214.5	46.5	87	6	US-11-080-991-24
767	214.5	46.5	116	4	US-10-161-493-34
768	209.5	45.4	86	4	US-10-161-493-32
769	191.5	41.5	113	4	US-10-205-823-142
770	191.5	41.5	113	4	US-10-177-293-168
771	191.5	41.5	113	4	US-10-295-027-1357
772	191.5	41.5	113	6	US-11-051-454-142
773	191.5	41.5	150	3	US-09-935-299-955

774	191.5	41.5	150	3	US-09-925-299-955	Sequence 955, App
775	129	28.0	92	3	US-09-981-876-238	Sequence 238, App
776	129	28.0	92	3	US-09-148-545-238	Sequence 238, App
777	129	28.0	92	3	US-09-903-190-120	Sequence 120, App
778	129	28.0	92	3	US-09-978-360A-776	Sequence 776, App
779	129	28.0	92	3	US-09-978-360A-776	Sequence 776, App
780	129	28.0	92	4	US-10-408-765A-1270	Sequence 1270, App
781	129	28.0	92	5	US-10-930-331-120	Sequence 120, App
782	129	28.0	92	5	US-10-979-111-238	Sequence 238, App
783	129	28.0	93	3	US-09-981-876-193	Sequence 183, App
784	129	28.0	93	3	US-09-148-545-193	Sequence 183, App
785	129	28.0	93	5	US-10-979-111-193	Sequence 183, App
786	121	26.2	70	3	US-09-981-876-269	Sequence 269, App
787	121	26.2	70	3	US-09-148-545-269	Sequence 269, App
788	121	26.2	70	5	US-10-979-111-269	Sequence 269, App
789	113.5	24.6	138	4	US-10-291-265-446	Sequence 446, App
790	113.5	24.6	138	6	US-11-000-463-446	Sequence 446, App
791	112.5	24.4	95	4	US-10-291-265-918	Sequence 918, App
792	112.5	24.4	95	6	US-11-000-463-918	Sequence 918, App
793	112.5	24.4	96	3	US-09-809-391-473	Sequence 473, App
794	112.5	24.4	96	3	US-09-882-171-473	Sequence 473, App
795	112.5	24.4	96	4	US-10-164-861-473	Sequence 473, App
796	112.5	24.4	96	6	US-11-144-947-473	Sequence 473, App
823	112.5	24.4	120	3	US-09-997-428-199	Sequence 199, App
1312	112.5	24.4	120	5	US-10-931-886-434	Sequence 434, App
1314	112.5	24.4	120	5	US-10-955-953-434	Sequence 434, App
1315	112.5	24.4	120	5	US-10-950-374-199	Sequence 199, App
1317	112.5	24.4	120	5	US-10-973-115B-434	Sequence 434, App
1320	112.5	24.4	120	6	US-11-290-153-434	Sequence 434, App
1321	106	23.0	69	3	US-09-809-391-606	Sequence 606, App
1322	106	23.0	69	3	US-09-882-171-606	Sequence 606, App
1328	106	23.0	69	4	US-10-164-861-606	Sequence 606, App
1324	106	23.0	69	6	US-11-144-947-606	Sequence 606, App
1325	105.5	22.9	110	5	US-10-450-763-56705	Sequence 56705, A
1326	94	20.4	115	4	US-10-352-272-2	Sequence 2, Appl
1327	94	20.4	178	3	US-09-833-245-1532	Sequence 1532, Ap
1328	94	20.4	178	3	US-09-985-153-92	Sequence 92, Appl
1329	94	20.4	178	3	US-09-985-153-93	Sequence 93, Appl
1330	94	20.4	178	3	US-09-985-153-94	Sequence 94, Appl
1331	94	20.4	178	3	US-09-985-153-96	Sequence 96, Appl

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Job time : 213 secs

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REFERENCE/DOCKET NUMBER: PF-0141 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 87 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 951423  
US-08-738-127-5

Query Match 55.6%; Score 256.5; DB 1; Length 87;  
Best Local Similarity 61.5%; Pred. No. 3.6e-25;  
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Db 1 MEGITCAFLVLAGLPVLEANGP-VDKGSPYYDWESLQLGGMIFGGLLCIAGIAMALSG 59  
Qy 60 KCKYKSSQKQHP--VPEKAIPLITPGSATT 88  
Db 60 KCK---CRNHTPSSLPEKVTPLITPGSAST 87

Search completed: November 21, 2006, 19:46:23  
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; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 461; DB 3; Length 89;
Best Local Similarity 100.0%; Pred. No. 2.2e-51;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERVTLALLLGLTALANDPFANKDDPFYDWNKQLSGLICGGLLAIAAGIAVLGSK 60
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DB 1 MERVTLALLLGLTALANDPFANKDDPFYDWNKQLSGLICGGLLAIAAGIAVLGSK 60
   |||||

QY 61 CKYKSSQKQHPVPEKAIPLTIPGSAATC 89
   |||||
DB 61 CKYKSSQKQHPVPEKAIPLTIPGSAATC 89
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RESULT 13
US-09-724-864-58
; Sequence 58, Application US/09724864
; Patent No. 6380362
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; TITLE OF INVENTION: Polynucleotides, polypeptides expressed
; FILE REFERENCE: 11000.1050U1
; CURRENT APPLICATION NUMBER: US/09/724,864
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Mouse
US-09-724-864-58

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Best Local Similarity 66.7%; Pred. No. 9.8e-28;
Matches 60; Conservative 8; Mismatches 19; Indels 3; Gaps 3;

QY 1 MERVTLA-LLLAGLTALEANDPFANKDDPFYDWNKQLSGLICGGLLAIAAGIAVLGSG 59
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DB 1 MBEITCAFLLLAGLPALEASDP-VDKDSFFYDWSLQGLIFGGLLCIAGIAWALGSG 59
   || : || ||||| ||||| : || ||||| : || ||||| : || |||||

QY 60 CKYKSSQKQHPVPEKAIPLTIPGSAATC 89
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DB 60 KCKCRTHKP-SLPGKATPLIPGSANTC 88
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RESULT 14
US-08-725-531-5
; Sequence 5, Application US/08725531
; Patent No. 5756310
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN PHOSPHOLEMMAN-LIKE PROTEIN
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.

; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/725,531
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0128 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 87 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 951423
US-08-725-531-5

Query Match      55.6%; Score 256.5; DB 1; Length 87;
Best Local Similarity 61.5%; Pred. No. 3.6e-25;
Matches 56; Conservative 11; Mismatches 17; Indels 7; Gaps 4;

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DB 1 MEGITCAFLVLAGLPVLEANGP-VDKGSFFYDWSLQGLMGWIFGGLLCIAGIAWALGSG 59
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QY 60 CKYKSSQKQHP--VPEKAIPLTIPGSAAT 88
   || : || ||||| ||||| : || ||||| : || ||||| : || |||||
DB 60 KCK---CRNHTPSSLPEKVTPLITPGSAST 87
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RESULT 15
US-08-738-127-5
; Sequence 5, Application US/08738127
; Patent No. 5919655
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hawkins, Phillip R.
; TITLE OF INVENTION: NOVEL HUMAN PHOSPHOLEMMAN HOMOLOG
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
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; OPERATING SYSTEM: DOS
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; APPLICATION NUMBER: US/08/738,127
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
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73	PRIOR FILING DATE: 1998-06-17

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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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Best Local Similarity 100.0%; Pred. No. 2.2e-51;
Matches      89; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1 MERVTLALLLLAGLTALEANDPFANKDDPFYVDWKNLQSLGTCGULLAAGTAAVLGSK 60
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QY      61 CRYKSSQKQHSVPPEKAIPLITPGSATTC 89
DB      61 CRYKSSQKQHSVPPEKAIPLITPGSATTC 89

RESULT 12
US-09-989-293A-262
; Sequence 262, Application US/09989293A
; Patent No. 7034136
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC66
; CURRENT APPLICATION NUMBER: US/09/989,293A
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
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; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910

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; PRIOR FILING DATE: 1998-07-02
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match          100.0%; Score 461; DB 3; Length 89;
Best Local Similarity 100.0%; Pred. No. 2.2e-51;
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QY 61 CKYSSKQHSPPVPEKAIPITPGSATTC 89
Db 61 CKYSSKQHSPPVPEKAIPITPGSATTC 89

RESULT 11
US-09-997-653-262
; Sequence 262, Application US/09997653
; Patent No. 7034122
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: KJavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PLC38
; CURRENT APPLICATION NUMBER: US/09/997,653
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/049787
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[illegible]

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; PRIOR FILING DATE: 1998-07-02
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 461; DB 3; Length 89;
Best Local Similarity 100.0%; Pred. No. 2.2e-51;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERVTLALLLGLTLEANDPFANKDDPFYDWKNLQSLGICGGLATAGTAAVLGK 60
DB 1 MERVTLALLLGLTLEANDPFANKDDPFYDWKNLQSLGICGGLATAGTAAVLGK 60

QY 61 CRYKSSQKQHSVPVEKAIPLITPGSATTC 89
DB 61 CRYKSSQKQHSVPVEKAIPLITPGSATTC 89

RESULT 10
US-09-997-349-262
; Sequence 262, Application US/09997349
; Patent No. 7034106
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P27301C37
; CURRENT APPLICATION NUMBER: US/09/997,349
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 461; DB 3; Length 89;
Best Local Similarity 100.0%; Pred. No. 2,2e-51;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 9
US-09-989-728-262
; Sequence 262, Application US/09989728
; Patent No. 7029873
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tuma, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C72
; CURRENT APPLICATION NUMBER: US/09/989,728
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 461; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 2.2e-51;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MERVTLALLLAGLTALEANDPFANKDDPPYDWNKQLSGLICGGLAATAGIAAVLSGK 60
Db 1 MERVTLALLLAGLTALEANDPFANKDDPPYDWNKQLSGLICGGLAATAGIAAVLSGK 60

Qy 61 CKYKSQKHSPVPEKAIPITGSATTC 89
Db 61 CKYKSQKHSPVPEKAIPITGSATTC 89

RESULT 7
US-09-389-726-262
; Sequence 262, Application US/09389726
; Patent No. 7018811
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC60

; CURRENT APPLICATION NUMBER: US/09/989,726
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; TITLE OF INVENTION: Acids Encoding the Same  
;; FILE REFERENCE: P27301C61  
;; CURRENT APPLICATION NUMBER: US/09/989,735  
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100

## RESULT 6

US-09-989-735-262

; Sequence 262, Application US/09989735

; Patent No. 6972185

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

**APPLICANT:** Ferrara, Napoleone

APPLICANT: Fong, Sherman

**APPLICANT:** Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Chris

APPLICANT: Gurney, Austin L.

APPLICANT: KIJAVIN, Ivar J.  
APPLICANT: Napien Mary A

APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James

APPLICANT: Paoni, James

APPLICANT: ROY, Margaret Ann  
APPLICANT: ROY, Nicholas F.

APPLICANT: ROY, Margaret Ann  
APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; PRIOR FILING DATE: 1998-06-25  
; PRIOR APPLICATION NUMBER: 60/090678  
; PRIOR FILING DATE: 1998-06-25  
; PRIOR APPLICATION NUMBER: 60/090690  
; PRIOR FILING DATE: 1998-06-25  
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Db 61 CKYSSQKHSPVPEKAIPITPGSATTC 89

#### RESULT 5

US-09-992-598-262

; Sequence 262, Application US/09992598

; Patent No. 6956108

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

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; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730P1C20  
; CURRENT APPLICATION NUMBER: US/09/992,598  
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APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumaas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
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;	PRIOR APPLICATION NUMBER:	60/091982	
;	PRIOR FILING DATE:	1998-07-07	
;	PRIOR APPLICATION NUMBER:	60/092182	
;	PRIOR FILING DATE:	1998-07-09	
Query Match 100.0%; Score 461;			
Best Local Similarity 100.0%; Pred. No. 2;			
Matches 89; Conservative 0; Mismatch			
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Db	1	MERVTLALLLGLTALFANDPFANKDDPFYFY	
Qy	61	CKYKSSQKHSPVPEKATPLITPGSATTG 89	
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RESULT 4			
US-09-997-333-262			
;	Sequence 262,	Application US/09997333	
;	Patent No. 6953836		
;	GENERAL INFORMATION:		
;	APPLICANT:	Ashkenazi, Avi J.	
;	APPLICANT:	Baker, Kevin P.	
;	APPLICANT:	Botstein, David	
;	APPLICANT:	Desnoyers, Luc	
;	APPLICANT:	Eaton, Dan L.	
;	APPLICANT:	Ferrara, Napoleone	
;	APPLICANT:	Fong, Sherman	
;	APPLICANT:	Gerber, Hanspeter	
;	APPLICANT:	Gerritsen, Mary E.	
;	APPLICANT:	Goddard, Audrey	
;	APPLICANT:	Godowski, Paul J.	
;	APPLICANT:	Grimaldi, J. Christopher	
;	APPLICANT:	Gurney, Austin L.	
;	APPLICANT:	Kljamin, Ivar J.	
;	APPLICANT:	Napier, Mary A.	
;	APPLICANT:	Pan, James	
;	APPLICANT:	Paoni, Nicholas F.	
;	APPLICANT:	Roy, Margaret Ann	



;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090542  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090557  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090676  
;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090678  
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;; PRIOR APPLICATION NUMBER: 60/090690  
;; PRIOR FILING DATE: 1998-06-25  
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;; PRIOR APPLICATION NUMBER: 60/091633  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 461; DB 2; Length 89;  
Best Local Similarity 100.0%; Pred. No. 2.2e-51;  
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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Db 1 MERVTLALLLGLTALEANDPFANKDDPFYDWNKQLSGLICGGLLAIAAGIAAVLSGK 60  
  
QY 61 CYKSSQKQHSVPPEKAIPLIITPGSATTC 89  
Db 61 CYKSSQKQHSVPPEKAIPLIITPGSATTC 89

RESULT 3  
US-09-990-444-262  
; Sequence 262, Application US/09990444  
; Patent No. 6930170  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.

;; APPLICANT: Pan, James  
;; APPLICANT: Paoni, Nicholas F.  
;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE OF INVENTION: Acids Encoding the Same  
;; FILE REFERENCE: P2730P1C19  
;; CURRENT APPLICATION NUMBER: US/09/990.444  
;; CURRENT FILING DATE: 2001-11-14  
;; PRIOR APPLICATION NUMBER: 60/049787  
;; PRIOR FILING DATE: 1997-06-16  
;; PRIOR APPLICATION NUMBER: 60/062250  
;; PRIOR FILING DATE: 1997-10-17  
;; PRIOR APPLICATION NUMBER: 60/065186  
;; PRIOR FILING DATE: 1997-11-12  
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;; PRIOR FILING DATE: 1998-04-28  
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;; PRIOR FILING DATE: 1998-05-07  
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;; PRIOR FILING DATE: 1998-06-02  
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;; PRIOR APPLICATION NUMBER: 60/088655  
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;; PRIOR APPLICATION NUMBER: 60/088738  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088742

APPLICANT: Gurney,Austin L.  
APPLICANT: Kljavin,Ivar J.  
APPLICANT: Napier,Mary A.  
APPLICANT: Pan,James  
APPLICANT: Paoni,Nicholas F.  
APPLICANT: Roy,Margaret Ann  
APPLICANT: Stewart,Timothy A.  
APPLICANT: Tumas,Daniel  
APPLICANT: Watanabe,Colin K.  
APPLICANT: Williams,P. Mickey  
APPLICANT: Wood,William I.  
APPLICANT: Zhang,Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730PIC53  
CURRENT APPLICATION NUMBER: US/09/991,181  
CURRENT FILING DATE: 2001-11-16  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
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PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090540

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1416	48	10.4	153	2	US-09-621-976-5179	Sequence 5179, Ap	1489	48	10.4	415	2	US-09-252-991A-30511	Sequence 30511, A
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1456	48	10.4	242	2	US-10-214-811-16	Sequence 16, Appl							
1457	48	10.4	242	2	US-10-766-074-16	Sequence 16, Appl							
1458	48	10.4	259	2	US-10-104-047-3858	Sequence 3858, Ap							
1459	48	10.4	260	2	US-09-252-991A-31125	Sequence 31125, A							
1460	48	10.4	267	2	US-09-780-016-12	Sequence 12, Appl							
1461	48	10.4	267	2	US-10-214-811-12	Sequence 12, Appl							
1462	48	10.4	267	2	US-10-766-074-12	Sequence 12, Appl							
1463	48	10.4	277	2	US-09-248-796A-17320	Sequence 17320, A							
1464	48	10.4	277	2	US-09-303-518D-402	Sequence 402, App							
1465	48	10.4	289	2	US-09-502-540-10736	Sequence 10736, A							
1466	48	10.4	295	2	US-09-870-956-4	Sequence 4, Appli							
1467	48	10.4	307	2	US-09-303-518D-404	Sequence 404, App							
1468	48	10.4	321	2	US-09-107-532A-4129	Sequence 4129, Ap							
1469	48	10.4	334	2	US-09-252-991A-31493	Sequence 31493, A							
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1473	48	10.4	342	2	US-09-146-661-3	Sequence 3, Appli							
1474	48	10.4	342	2	US-09-150-515-3	Sequence 3, Appli							
1475	48	10.4	342	2	US-09-328-352-7250	Sequence 7250, Ap							
1476	48	10.4	356	1	US-08-700-607-6	Sequence 6, Appli							
1477	48	10.4	357	2	US-09-252-991A-24149	Sequence 24149, A							
1478	48	10.4	360	2	US-09-107-532A-4523	Sequence 4523, Ap							
1479	48	10.4	362	2	US-09-949-016-8242	Sequence 8242, Ap							
1480	48	10.4	375	2	US-09-614-512-96	Sequence 96, Appl							
1481	48	10.4	376	2	US-09-543-681A-8277	Sequence 8277, Ap							
1482	48	10.4	392	2	US-09-270-767-59402	Sequence 59402, A							
1483	48	10.4	397	2	US-09-605-703B-1912	Sequence 1912, Ap							
1484	48	10.4	401	2	US-09-328-352-5448	Sequence 5448, Ap							
1485	48	10.4	406	2	US-09-252-991A-28543	Sequence 28543, A							
1486	48	10.4	407	2	US-09-549-848B-4	Sequence 4, Appli							

ALIGNMENTS

RESULT 1

US-09-289-349-11  
; Sequence 11, Application US/09289349  
; Patent No. 6277574  
; GENERAL INFORMATION:  
; APPLICANT: Walker, Michael, G.  
; APPLICANT: Volkumuth, Wayne  
; APPLICANT: Klinger, Tod, M.  
; APPLICANT: Azimzai, Yalda  
; APPLICANT: Yue, Henry  
; TITLE OF INVENTION: GENES ASSOCIATED WITH DISEASES OF THE KIDNEY  
; FILE REFERENCE: PB-0010 US  
; CURRENT APPLICATION NUMBER: US/09/289,349  
; CURRENT FILING DATE: 1999-04-09  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PERL Program  
; SEQ ID NO 11  
; LENGTH: 89  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE: -  
; OTHER INFORMATION: 1900433CD1  
US-09-289-349-11

Query Match 100.0%; Score 461; DB 2; Length 89;  
Best Local Similarity 100.0%; Pred. No. 2.2e-51;  
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERVTLALLLLAGLTAALEANDPFANKDDPPFYDWNKLNQLSGLICGGLLAAGTAAVLSGK 60  
Db 1 MERVTLALLLLAGLTAALEANDPFANKDDPPFYDWNKLNQLSGLICGGLLAAGTAAVLSGK 60  
QY 61 CKYKSSQKHSPVPEKAIPITPGSATTC 89  
Db 61 CKYKSSQKHSPVPEKAIPITPGSATTC 89

RESULT 2

US-09-991-181-262  
; Sequence 262, Application US/09991181  
; Patent No. 6913919  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
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1268	48.5	10.5	114	2	US-09-054-711C-5	Sequence 5, Appli	1341	48.5	10.5	258	2	US-09-315-574-5	Sequence 5, Appli
1269	48.5	10.5	114	2	US-09-679-710B-1	Sequence 1, Appli	1342	48.5	10.5	279	2	US-08-328-352-4717	Sequence 4717, Ap
1270	48.5	10.5	114	2	US-09-679-710B-2	Sequence 2, Appli	1343	48.5	10.5	285	2	US-08-992-035A-1	Sequence 1, Appli
1271	48.5	10.5	114	2	US-09-679-710B-3	Sequence 3, Appli	1344	48.5	10.5	285	2	US-09-252-991A-32954	Sequence 32954, A
1272	48.5	10.5	114	2	US-09-679-710B-4	Sequence 4, Appli	1345	48.5	10.5	293	2	US-09-660-587-40	Sequence 40, Appl
1273	48.5	10.5	114	2	US-09-679-710B-5	Sequence 5, Appli	1346	48.5	10.5	293	2	US-09-314-701-44	Sequence 44, Appl
1274	48.5	10.5	114	2	US-09-679-710B-6	Sequence 6, Appli	1347	48.5	10.5	293	2	US-09-811-007A-40	Sequence 40, Appl
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1276	48.5	10.5	114	2	US-09-679-710B-8	Sequence 8, Appli	1349	48.5	10.5	293	2	US-10-059-964A-44	Sequence 44, Appl
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1291	48.5	10.5	114	2	US-09-938-936-1	Sequence 1, Appli	1364	48.5	10.5	494	2	US-09-543-681A-7033	Sequence 7033, Ap
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1302	48.5	10.5	114	2	US-10-053-406-7	Sequence 7, Appli	1375	48.5	10.5	599	2	US-10-407-339-1	Sequence 1, Appli
1303	48.5	10.5	114	2	US-10-053-406-8	Sequence 8, Appli	1376	48.5	10.5	608	2	US-09-769-787-8	Sequence 8, Appli
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1317	48.5	10.5	114	2	US-10-053-406-22	Sequence 22, Appl	1390	48.5	10.5	1278	2	US-09-134-000C-6043	Sequence 6043, Ap
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1320	48.5	10.5	132	2	US-09-462-941-19	Sequence 19, Appl	1393	48.5	10.5	1884	2	US-09-538-092-1329	Sequence 1329, Ap
1321	48.5	10.5	132	2	US-09-949-016-6187	Sequence 6187, Ap	1394	48.5	10.5	4545	1	US-08-804-227C-14	Sequence 14, Appl
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1329	48.5	10.5	157	2	US-09-378-238-31	Sequence 31, Appl	1402	48.5	10.4	74	2	US-09-489-847-300	Sequence 229, App
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1336	48.5	10.5	247	1	US-07-885-089B-8	Sequence 8, Appli	1409	48.5	10.4	133	2	US-10-206-576-226	Sequence 226, App
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1126	49	10.6	118	2	US-09-072-596-226	Sequence 226, App	1199	49	10.6	428	2	US-09-248-796A-20582	Sequence 20582, A
1127	49	10.6	118	2	US-09-072-967-231	Sequence 231, App	1200	49	10.6	436	2	US-09-134-000C-4843	Sequence 4843, Ap
1128	49	10.6	118	2	US-10-193-003-226	Sequence 226, App	1201	49	10.6	454	2	US-09-270-767-45646	Sequence 45646, A
1129	49	10.6	118	2	US-10-084-843-231	Sequence 231, App	1202	49	10.6	463	1	US-08-677-049-6	Sequence 6, Appli
1130	49	10.6	156	2	US-09-134-001C-4234	Sequence 4234, Ap	1203	49	10.6	464	2	US-09-252-991A-26212	Sequence 26212, A
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1139	49	10.6	195	2	US-09-635-359B-24	Sequence 24, Appl	1212	49	10.6	526	2	US-09-543-681A-6631	Sequence 6631, A
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1143	49	10.6	219	2	US-10-115-123-151	Sequence 151, App	1216	49	10.6	629	5	PCT-US92-09382-8	Sequence 8, Appli
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1145	49	10.6	230	2	US-09-134-000C-5011	Sequence 5011, Ap	1218	49	10.6	644	2	US-09-949-016-9507	Sequence 9507, Ap
1146	49	10.6	231	2	US-09-893-737-154	Sequence 154, App	1219	49	10.6	649	2	US-09-248-796A-20641	Sequence 20641, A
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1148	49	10.6	239	2	US-08-913-014A-3	Sequence 3, Appli	1221	49	10.6	659	2	US-09-228-986-75	Sequence 75, Appl
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1154	49	10.6	262	2	US-09-956-087-4	Sequence 4, Appli	1227	49	10.6	722	2	US-09-949-016-6418	Sequence 6418, Ap
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1157	49	10.6	274	2	US-09-420-592A-7	Sequence 7, Appli	1230	49	10.6	742	2	US-09-949-016-11569	Sequence 11569, A
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1165	49	10.6	342	2	US-08-785-928-1	Sequence 1, Appli	1238	49	10.6	908	2	US-09-986-552-15	Sequence 15, Appl
1166	49	10.6	342	2	US-08-728-603-17	Sequence 17, Appl	1239	49	10.6	908	2	US-09-636-596C-15	Sequence 15, Appl
1167	49	10.6	345	2	US-09-328-352-4841	Sequence 4841, Ap	1240	49	10.6	908	2	US-10-023-884-9	Sequence 9, Appli
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1169	49	10.6	349	2	US-08-630-172-6	Sequence 6, Appli	1242	49	10.6	908	2	US-09-895-072-15	Sequence 15, Appl
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1174	49	10.6	352	2	US-08-861-105-14	Sequence 14, Appl	1247	49	10.6	914	2	US-10-270-595-6	Sequence 6, Appli
1175	49	10.6	352	2	US-08-575-967A-2	Sequence 2, Appli	1248	49	10.6	946	2	US-09-902-540-16817	Sequence 16817, A
1176	49	10.6	352	2	US-09-045-583-52	Sequence 52, Appl	1249	49	10.6	984	1	US-09-409-604-4	Sequence 4, Appli
1177	49	10.6	352	2	US-09-517-605-5	Sequence 5, Appli	1250	49	10.6	1070	2	US-08-633-770A-2	Sequence 2, Appli
1178	49	10.6	352	2	US-09-534-185-52	Sequence 52, Appl	1251	49	10.6	1070	2	US-09-280-197-6	Sequence 6, Appli
1179	49	10.6	352	2	US-08-833-752-5	Sequence 5, Appli	1252	49	10.6	1070	2	US-09-423-126-4	Sequence 4, Appli
1180	49	10.6	352	2	US-09-502-783A-2	Sequence 2, Appli	1253	49	10.6	1073	2	US-09-180-245-2	Sequence 2, Appli
1181	49	10.6	352	2	US-09-796-202-1	Sequence 1, Appli	1254	49	10.6	1073	2	US-09-819-249-2	Sequence 2, Appli
1182	49	10.6	352	2	US-09-938-719-5	Sequence 5, Appli	1255	49	10.6	1089	2	US-09-866-510-4	Sequence 4, Appli
1183	49	10.6	352	2	US-09-502-783A-2	Sequence 2, Appli	1256	49	10.6	1200	2	US-10-094-749-2682	Sequence 2682, Ap
1184	49	10.6	352	2	US-09-339-912A-2	Sequence 2, Appli	1257	49	10.6	1566	2	US-10-152-866-23	Sequence 23, Appl
1185	49	10.6	352	2	US-08-771-276-2	Sequence 2, Appli	1258	48.5	10.5	27	2	US-09-962-756-1637	Sequence 1637, Ap
1186	49	10.6	352	2	US-08-771-276-20	Sequence 20, Appl	1259	48.5	10.5	51	1	US-10-067-422-18	Sequence 18, Appl
1187	49	10.6	352	2	US-09-939-226B-5	Sequence 5, Appli	1260	48.5	10.5	57	1	US-08-358-160-103	Sequence 103, App
1188	49	10.6	352	2	US-09-135-662A-2	Sequence 2, Appli	1261	48.5	10.5	77	2	US-09-781-988A-283	Sequence 283, App
1189	49	10.6	352	2	US-09-949-002-303	Sequence 303, App	1262	48.5	10.5	94	2	US-08-311-731A-385	Sequence 385, App
1190	49	10.6	352	2	US-10-323-314-1	Sequence 1, Appli	1263	48.5	10.5	94	2	US-09-252-991A-29771	Sequence 29771, A
1191	49	10.6	352	2	US-09-938-703B-5	Sequence 5, Appli	1264	48.5	10.5	112	1	US-08-284-393B-4	Sequence 4, Appli
1192	49	10.6	352	2	US-10-072-301A-1	Sequence 1, Appli	1265	48.5	10.5	112	1	US-08-284-393B-14	Sequence 14, Appl
1193	49	10.6	357	2	US-09-949-016-9074	Sequence 9074, Ap	1266	48.5	10.5	112	5	PCT-US95-08950-4	Sequence 4, Appli
1194	49	10.6	358	2	US-09-543-681A-4765	Sequence 4765, Ap	1267	48.5	10.5	114	2	US-09-054-711C-4	Sequence 4, Appli

976	50	10.8	501	2	US-09-252-991A-31885	Sequence 31885, A	1049	49.5	10.7	394	2	US-09-710-279-3292	Sequence 3292, Ap
977	50	10.8	521	2	US-09-134-001C-4290	Sequence 4290, Ap	1050	49.5	10.7	403	2	US-09-489-039A-11022	Sequence 11022, A
978	50	10.8	525	2	US-09-949-016-7407	Sequence 7407, Ap	1051	49.5	10.7	414	2	US-09-710-279-806	Sequence 806, App
979	50	10.8	533	2	US-09-549-519-31	Sequence 31, Appl	1052	49.5	10.7	420	2	US-09-252-991A-30428	Sequence 30428, A
980	50	10.8	544	2	US-09-252-991A-26096	Sequence 26096, A	1053	49.5	10.7	423	2	US-09-134-001C-3599	Sequence 3599, Ap
981	50	10.8	605	2	US-09-949-016-8269	Sequence 8269, Ap	1054	49.5	10.7	427	2	US-09-328-352-6602	Sequence 6602, Ap
982	50	10.8	606	2	US-09-538-092-798	Sequence 798, App	1055	49.5	10.7	432	2	US-09-902-540-9717	Sequence 9717, Ap
983	50	10.8	641	2	US-09-653-274-13	Sequence 13, Appl	1056	49.5	10.7	436	2	US-09-886-319A-72	Sequence 72, Appl
984	50	10.8	641	2	US-10-461-791-13	Sequence 13, Appl	1057	49.5	10.7	463	2	US-08-753-007A-8	Sequence 8, Appli
985	50	10.8	772	2	US-09-252-991A-30446	Sequence 30446, A	1058	49.5	10.7	469	2	US-09-398-496-8	Sequence 8, Appli
986	50	10.8	970	2	US-09-979-195-10	Sequence 10, Appl	1059	49.5	10.7	470	2	US-10-104-047-3775	Sequence 3775, Ap
987	50	10.8	1070	2	US-09-653-274-8	Sequence 8, Appli	1060	49.5	10.7	476	2	US-09-134-001C-3778	Sequence 3778, Ap
988	50	10.8	1070	2	US-10-461-791-8	Sequence 8, Appli	1061	49.5	10.7	478	2	US-09-248-796A-15018	Sequence 15018, A
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990	50	10.8	1086	2	US-10-461-791-4	Sequence 4, Appli	1063	49.5	10.7	507	2	US-10-214-811-2	Sequence 2, Appli
991	50	10.8	1309	2	US-09-862-027-82	Sequence 82, Appli	1064	49.5	10.7	532	2	US-10-766-074-2	Sequence 2, Appli
992	50	10.8	1381	2	US-08-826-134-4	Sequence 4, Appli	1065	49.5	10.7	532	2	US-09-780-016-20	Sequence 20, Appl
993	50	10.8	1443	1	US-08-308-872B-2	Sequence 2, Appli	1066	49.5	10.7	532	2	US-10-214-811-20	Sequence 20, Appl
994	50	10.8	1479	2	US-08-840-062-2	Sequence 2, Appli	1067	49.5	10.7	532	2	US-10-766-074-20	Sequence 20, Appl
995	49.5	10.7	58	1	US-08-721-745-2	Sequence 2, Appli	1068	49.5	10.7	556	2	US-09-907-794A-259	Sequence 259, App
996	49.5	10.7	59	2	US-09-513-999C-5346	Sequence 5346, Ap	1069	49.5	10.7	556	2	US-08-905-125A-259	Sequence 259, App
997	49.5	10.7	66	2	US-09-513-999C-7224	Sequence 7224, Ap	1070	49.5	10.7	556	2	US-09-902-775A-259	Sequence 259, App
998	49.5	10.7	160	2	US-09-732-210-304	Sequence 304, App	1071	49.5	10.7	556	2	US-09-906-700-259	Sequence 259, App
999	49.5	10.7	160	2	US-09-107-532A-5111	Sequence 5111, Ap	1072	49.5	10.7	556	2	US-09-903-603A-259	Sequence 259, App
1000	49.5	10.7	172	2	US-08-772-270A-1	Sequence 1, Appl	1073	49.5	10.7	556	2	US-09-904-920A-259	Sequence 259, App
1001	49.5	10.7	172	2	US-09-062-126-2	Sequence 2, Appli	1074	49.5	10.7	556	2	US-09-909-064-259	Sequence 259, App
1002	49.5	10.7	193	2	US-09-475-316A-78	Sequence 78, Appl	1075	49.5	10.7	556	2	US-09-905-381A-259	Sequence 259, App
1003	49.5	10.7	193	2	US-09-704-640-78	Sequence 78, Appl	1076	49.5	10.7	556	2	US-09-906-618-259	Sequence 259, App
1004	49.5	10.7	200	1	US-08-698-805-6	Sequence 6, Appli	1077	49.5	10.7	556	2	US-09-906-646-259	Sequence 259, App
1005	49.5	10.7	212	2	US-09-813-453B-59	Sequence 59, Appl	1078	49.5	10.7	556	2	US-09-904-462-259	Sequence 259, App
1006	49.5	10.7	226	2	US-10-094-749-2249	Sequence 2249, Ap	1079	49.5	10.7	556	2	US-09-902-736A-259	Sequence 259, App
1007	49.5	10.7	246	2	US-09-134-001C-5292	Sequence 5292, Ap	1080	49.5	10.7	556	2	US-09-906-722A-259	Sequence 259, App
1008	49.5	10.7	249	1	US-08-626-685A-11	Sequence 11, Appl	1081	49.5	10.7	556	2	US-09-905-449-259	Sequence 259, App
1009	49.5	10.7	249	2	US-09-248-796A-19210	Sequence 7, Appli	1082	49.5	10.7	556	2	US-09-903-562B-259	Sequence 259, App
1010	49.5	10.7	252	1	US-07-885-089B-7	Sequence 7, Appli	1083	49.5	10.7	556	2	US-09-906-679A-259	Sequence 259, App
1011	49.5	10.7	252	2	US-09-919-039-228	Sequence 228, App	1084	49.5	10.7	556	3	US-09-907-841-259	Sequence 259, App
1012	49.5	10.7	252	2	US-09-919-039-228	Sequence 228, App	1085	49.5	10.7	557	2	US-10-771-708-4	Sequence 4, Appli
1013	49.5	10.7	262	2	US-09-134-001C-3746	Sequence 3746, Ap	1086	49.5	10.7	563	2	US-08-931-608A-3	Sequence 3, Appli
1014	49.5	10.7	262	2	US-09-710-279-1568	Sequence 1568, Ap	1087	49.5	10.7	563	2	US-08-851-847-3	Sequence 3, Appli
1015	49.5	10.7	265	2	US-09-780-016-8	Sequence 8, Appli	1088	49.5	10.7	582	2	US-09-252-991A-21510	Sequence 21510, A
1016	49.5	10.7	265	2	US-10-214-811-8	Sequence 8, Appli	1089	49.5	10.7	597	2	US-09-252-991A-32657	Sequence 32657, A
1017	49.5	10.7	265	2	US-10-766-074-8	Sequence 8, Appli	1090	49.5	10.7	607	2	US-09-252-991A-32643	Sequence 32643, A
1018	49.5	10.7	268	2	US-09-716-964B-156	Sequence 156, App	1091	49.5	10.7	637	2	US-09-569-611C-35	Sequence 35, Appl
1019	49.5	10.7	290	2	US-09-780-016-6	Sequence 6, Appli	1092	49.5	10.7	637	2	US-08-753-007A-32	Sequence 32, Appl
1020	49.5	10.7	290	2	US-10-214-811-6	Sequence 6, Appli	1093	49.5	10.7	647	2	US-08-398-456-32	Sequence 32, Appl
1021	49.5	10.7	290	2	US-10-766-074-6	Sequence 6, Appli	1094	49.5	10.7	660	2	US-09-907-794A-28	Sequence 28, Appl
1022	49.5	10.7	296	2	US-09-489-847-293	Sequence 293, App	1095	49.5	10.7	660	2	US-09-905-125A-28	Sequence 28, Appl
1023	49.5	10.7	315	2	US-09-107-532A-28066	Sequence 28066, A	1096	49.5	10.7	660	2	US-09-902-775A-28	Sequence 28, Appl
1024	49.5	10.7	319	2	US-09-252-991A-28066	Sequence 28066, A	1097	49.5	10.7	660	2	US-09-906-700-28	Sequence 28, Appl
1025	49.5	10.7	320	2	US-09-489-039A-10349	Sequence 10349, A	1098	49.5	10.7	660	2	US-09-903-603A-28	Sequence 28, Appl
1026	49.5	10.7	322	2	US-09-949-016-11381	Sequence 11381, A	1099	49.5	10.7	660	2	US-09-904-920A-28	Sequence 28, Appl
1027	49.5	10.7	324	2	US-09-602-787A-484	Sequence 484, App	1100	49.5	10.7	660	2	US-09-949-016-6843	Sequence 6843, Ap
1028	49.5	10.7	328	2	US-09-605-703B-2840	Sequence 2840, Ap	1101	49.5	10.7	660	2	US-09-905-064-28	Sequence 28, Appl
1029	49.5	10.7	353	2	US-09-489-039A-12270	Sequence 12270, A	1102	49.5	10.7	660	2	US-09-905-381A-28	Sequence 28, Appl
1030	49.5	10.7	363	2	US-09-949-016-11040	Sequence 11040, A	1103	49.5	10.7	660	2	US-09-906-618-28	Sequence 28, Appl
1031	49.5	10.7	364	2	US-09-489-039A-10066	Sequence 10066, A	1104	49.5	10.7	660	2	US-09-906-646-28	Sequence 28, Appl
1032	49.5	10.7	372	1	US-08-626-685A-8	Sequence 8, Appli	1105	49.5	10.7	660	2	US-08-689-486-38	Sequence 38, Appl
1033	49.5	10.7	372	2	US-08-993-088A-2	Sequence 2, Appli	1106	49.5	10.7	660	2	US-09-904-462-28	Sequence 28, Appl
1034	49.5	10.7	372	2	US-08-993-088A-20	Sequence 20, Appli	1107	49.5	10.7	660	2	US-09-902-736A-28	Sequence 28, Appl
1035	49.5	10.7	372	2	US-08-993-424B-2	Sequence 2, Appli	1108	49.5	10.7	660	2	US-09-906-722A-28	Sequence 28, Appl
1036	49.5	10.7	372	2	US-08-665-034A-2	Sequence 2, Appli	1109	49.5	10.7	660	2	US-09-905-449-28	Sequence 28, Appl
1037	49.5	10.7	372	2	US-08-665-034A-4	Sequence 4, Appli	1110	49.5	10.7	660	2	US-09-903-562B-28	Sequence 28, Appl
1038	49.5	10.7	372	2	US-09-595-549-9	Sequence 9, Appli	1111	49.5	10.7	660	2	US-09-906-679A-28	Sequence 28, Appl
1039	49.5	10.7	372	2	US-09-603-680-2	Sequence 2, Appli	1112	49.5	10.7	660	2	US-09-973-424A-58	Sequence 58, Appl
1040	49.5	10.7	372	2	US-09-603-680-20	Sequence 20, Appli	1113	49.5	10.7	661	3	US-09-907-841-28	Sequence 28, Appl
1041	49.5	10.7	372	2	US-08-981-700A-2	Sequence 2, Appli	1114	49.5	10.7	661	2	US-09-252-991A-27070	Sequence 27070, A
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1043	49.5	10.7	372	2	US-09-011-553-2	Sequence 2, Appli	1116	49.5	10.7	683	2	US-09-949-016-7267	Sequence 7267, Ap
1044	49.5	10.7	378	2	US-09-689-486-62	Sequence 62, Appli	1117	49.5	10.7	741	2	US-09-252-991A-22440	Sequence 22440, A
1045	49.5	10.7	378	2	US-09-973-424A-62	Sequence 62, Appl	1118	49.5	10.7	770	2	US-09-538-092-1265	Sequence 1265, Ap
1046	49.5	10.7	380	2	US-09-120-365-76	Sequence 76, Appl	1119	49.5	10.7	1121	2	US-08-915-048A-2	Sequence 2, Appli
1047	49.5	10.7	380	2	US-09-515-039-76	Sequence 76, Appl	1120	49.5	10.7	2446	2	US-09-949-016-11439	Sequence 11439, A
1048	49.5	10.7	380	2	US-08-860-255A-5	Sequence 5, Appli	1121	49	10.6	63	2	US-09-471-276-1429	Sequence 1429, Ap

830	51	11.1	1093	2	US-09-854-845-4	Sequence 4, Appli	903	50.5	11.0	1163	1	US-08-482-293A-4	Sequence 4, Appli
831	51	11.1	1151	2	US-09-854-845-10	Sequence 10, Appl	904	50.5	11.0	1163	1	US-08-943-363-4	Sequence 4, Appli
832	51	11.1	1479	2	US-08-840-062-4	Sequence 4, Appli	905	50.5	11.0	1163	1	US-08-476-062A-44	Sequence 44, Appl
833	51	11.1	1956	2	US-08-843-417-10	Sequence 10, Appl	906	50.5	11.0	1163	1	US-08-193-043-4	Sequence 4, Appli
834	51	11.1	1956	2	US-09-527-013-10	Sequence 10, Appl	907	50.5	11.0	1163	2	US-09-688-307A-4	Sequence 4, Appli
835	50.5	11.0	26	2	US-09-962-756-1658	Sequence 1658, Ap	908	50.5	11.0	1163	2	US-09-350-259-4	Sequence 44, Appl
836	50.5	11.0	87	2	US-09-605-703B-960	Sequence 960, App	909	50.5	11.0	1163	5	PCT-US96-01314-44	Sequence 5, Appli
837	50.5	11.0	87	2	US-09-605-703B-962	Sequence 962, App	910	50.5	11.0	1211	2	US-09-491-522-5	Sequence 5, Appli
838	50.5	11.0	142	2	US-10-104-047-2706	Sequence 2706, Ap	911	50.5	11.0	1211	2	US-09-949-016-11401	Sequence 11401, A
839	50.5	11.0	147	2	US-09-543-681A-4506	Sequence 4506, Ap	912	50.5	11.0	1211	2	US-09-949-002-401	Sequence 401, App
840	50.5	11.0	188	1	US-08-160-524A-5	Sequence 5, Appli	913	50.5	11.0	1211	2	US-09-949-002-555	Sequence 555, App
841	50.5	11.0	207	1	US-08-609-443B-15	Sequence 15, Appl	914	50.5	11.0	1245	2	US-09-252-921A-30935	Sequence 30935, A
842	50.5	11.0	207	2	US-08-569-063C-15	Sequence 15, Appl	915	50.5	11.0	1317	2	US-09-083-521-7	Sequence 7, Appli
843	50.5	11.0	207	2	US-08-851-896-15	Sequence 15, Appl	916	50.5	11.0	2703	1	US-08-185-432-19	Sequence 19, Appl
844	50.5	11.0	249	2	US-09-583-110-4357	Sequence 4357, Ap	917	50.5	11.0	2703	2	US-08-899-232-4	Sequence 4, Appli
845	50.5	11.0	249	2	US-09-602-777A-344	Sequence 344, App	918	50.5	11.0	2703	2	US-08-121-457-4	Sequence 4, Appli
846	50.5	11.0	254	2	US-09-107-433-4333	Sequence 4333, Ap	919	50.5	11.0	3169	1	US-08-477-451-6	Sequence 6, Appli
847	50.5	11.0	255	2	US-09-605-703B-244	Sequence 244, App	920	50	10.8	31	2	US-09-270-767-52626	Sequence 37409, A
848	50.5	11.0	263	2	US-09-605-703B-242	Sequence 242, App	921	50	10.8	31	2	US-09-270-767-52626	Sequence 52626, A
849	50.5	11.0	264	1	US-08-463-115-93	Sequence 93, Appl	922	50	10.8	69	2	US-09-248-796A-27038	Sequence 27038, A
850	50.5	11.0	264	1	US-08-465-388-93	Sequence 93, Appl	923	50	10.8	92	2	US-09-127-946-8	Sequence 8, Appli
851	50.5	11.0	271	2	US-09-252-991A-18965	Sequence 18965, A	924	50	10.8	92	2	US-09-148-545-256	Sequence 256, App
852	50.5	11.0	304	2	US-09-902-540-13353	Sequence 13353, A	925	50	10.8	93	2	US-09-621-011-256	Sequence 256, App
853	50.5	11.0	306	2	US-09-252-991A-22181	Sequence 22181, A	926	50	10.8	102	2	US-09-198-452A-475	Sequence 475, App
854	50.5	11.0	326	2	US-09-328-352-5506	Sequence 5506, Ap	927	50	10.8	105	2	US-09-248-796A-19711	Sequence 19711, A
855	50.5	11.0	349	2	US-09-949-016-9786	Sequence 9786, Ap	928	50	10.8	119	2	US-09-482-273-264	Sequence 264, App
856	50.5	11.0	355	2	US-08-984-618-14	Sequence 14, Appl	929	50	10.8	147	2	US-09-902-540-12970	Sequence 12970, A
857	50.5	11.0	364	2	US-09-829-275-1	Sequence 1, Appli	930	50	10.8	195	2	US-09-394-142B-16	Sequence 16, Appl
858	50.5	11.0	377	1	US-08-188-277B-80	Sequence 80, Appl	931	50	10.8	201	2	US-09-270-767-31650	Sequence 31650, A
859	50.5	11.0	377	1	US-08-429-964-8	Sequence 80, Appl	932	50	10.8	201	2	US-09-270-767-46867	Sequence 46867, A
860	50.5	11.0	385	2	US-09-107-532A-5871	Sequence 5871, Ap	933	50	10.8	243	2	US-10-094-749-3240	Sequence 3240, Ap
861	50.5	11.0	411	2	US-09-107-532A-5966	Sequence 5966, Ap	934	50	10.8	248	2	US-09-634-238-279	Sequence 279, App
862	50.5	11.0	424	2	US-09-902-540-10575	Sequence 10575, A	935	50	10.8	252	2	US-09-902-540-12546	Sequence 12546, A
863	50.5	11.0	426	2	US-09-902-540-14942	Sequence 14942, A	936	50	10.8	261	2	US-09-543-681A-5280	Sequence 5280, Ap
864	50.5	11.0	433	2	US-09-902-540-13296	Sequence 13296, A	937	50	10.8	263	2	US-09-328-352-4486	Sequence 4486, Ap
865	50.5	11.0	442	2	US-09-538-092-637	Sequence 637, App	938	50	10.8	264	2	US-09-198-452A-266	Sequence 266, App
866	50.5	11.0	455	2	US-09-543-681A-7043	Sequence 7043, App	939	50	10.8	267	2	US-09-134-000C-6206	Sequence 6206, Ap
867	50.5	11.0	461	2	US-09-107-532A-5964	Sequence 5964, Ap	940	50	10.8	273	2	US-09-489-039A-12374	Sequence 12374, A
868	50.5	11.0	476	2	US-09-902-540-11298	Sequence 11298, A	941	50	10.8	277	2	US-09-303-518D-400	Sequence 400, App
869	50.5	11.0	476	2	US-10-142-835-28	Sequence 28, Appl	942	50	10.8	279	2	US-09-134-001C-4878	Sequence 4878, Ap
870	50.5	11.0	477	2	US-09-252-991A-29825	Sequence 29825, A	943	50	10.8	303	2	US-09-543-681A-5154	Sequence 5154, Ap
871	50.5	11.0	498	2	US-09-252-991A-27221	Sequence 27221, A	945	50	10.8	308	1	US-08-164-292B-18	Sequence 18, Appl
872	50.5	11.0	529	1	US-07-891-942C-8	Sequence 8, Appli	946	50	10.8	308	2	US-08-845-623-18	Sequence 18, Appl
873	50.5	11.0	529	1	US-08-370-909-19	Sequence 19, Appl	947	50	10.8	308	2	US-08-815-927-18	Sequence 18, Appl
874	50.5	11.0	529	1	US-08-504-048-8	Sequence 8, Appli	948	50	10.8	308	2	US-09-103-330-18	Sequence 18, Appl
875	50.5	11.0	529	2	US-09-341-982-1	Sequence 1, Appli	949	50	10.8	308	2	US-09-435-242-18	Sequence 18, Appl
876	50.5	11.0	529	2	US-09-169-717B-39	Sequence 39, Appl	950	50	10.8	308	3	US-10-046-938-18	Sequence 18, Appl
877	50.5	11.0	529	2	US-10-011-436-4	Sequence 4, Appli	951	50	10.8	322	2	US-09-252-991A-24657	Sequence 24657, A
878	50.5	11.0	529	2	US-08-533-895A-39	Sequence 39, Appl	952	50	10.8	323	2	US-09-107-532A-6263	Sequence 6263, Ap
879	50.5	11.0	529	3	US-08-816-454B-232	Sequence 292, App	953	50	10.8	326	2	US-09-784-810C-11	Sequence 11, Appl
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881	50.5	11.0	550	1	US-08-279-700-18	Sequence 18, Appl	955	50	10.8	352	2	US-10-044-564-100	Sequence 100, App
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883	50.5	11.0	550	1	US-08-279-700-22	Sequence 22, Appl	957	50	10.8	356	2	US-09-125-619-13	Sequence 13, Appl
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887	50.5	11.0	566	2	US-09-949-016-8505	Sequence 8505, Ap	961	50	10.8	356	2	US-10-143-024A-13	Sequence 13, Appl
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891	50.5	11.0	596	2	US-09-252-991A-22689	Sequence 22689, A	965	50	10.8	378	2	US-09-902-540-11860	Sequence 11860, A
892	50.5	11.0	614	2	US-09-949-016-10772	Sequence 10772, A	966	50	10.8	390	2	US-09-710-279-1422	Sequence 1422, Ap
893	50.5	11.0	757	2	US-09-902-540-11380	Sequence 11380, A	967	50	10.8	427	2	US-09-902-540-15413	Sequence 15413, A
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895	50.5	11.0	974	2	US-08-938-291A-4	Sequence 4, Appli	969	50	10.8	440	2	US-08-584-760A-1	Sequence 1, Appli
896	50.5	11.0	974	2	US-09-589-619-4	Sequence 4, Appli	970	50	10.8	447	2	US-10-162-012-29	Sequence 29, Appl
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899	50.5	11.0	1163	1	US-08-286-889-4	Sequence 4, Appli	973	50	10.8	468	3	US-09-497-967-7	Sequence 7, Appli
900	50.5	11.0	1163	1	US-08-485-618-4	Sequence 4, Appli	974	50	10.8	468	3	US-09-497-967-54	Sequence 54, Appl
901	50.5	11.0	1163	1	US-08-362-652-4	Sequence 4, Appli	975	50	10.8	471	2	US-09-784-810C-6	Sequence 6, Appli
902	50.5	11.0	1163	1	US-08-605-672-4	Sequence 4, Appli							



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686	51.5	11.2	307	2	US-10-015-389A-95	Sequence 95, Appl	759	51.5	11.2	1454	5	PCT-US93-04384-46	Sequence 46, Appl
687	51.5	11.2	307	2	US-10-006-768A-95	Sequence 95, Appl	760	51.5	11.2	1454	5	PCT-US93-04384-47	Sequence 47, Appl
688	51.5	11.2	307	2	US-10-015-371A-95	Sequence 95, Appl	761	51.5	11.2	2539	2	US-09-413-814-42	Sequence 42, Appl
689	51.5	11.2	307	2	US-10-015-391A-95	Sequence 95, Appl	762	51	11.1	86	2	US-08-654-737B-2	Sequence 2, Appl
690	51.5	11.2	307	2	US-10-011-833A-95	Sequence 95, Appl	763	51	11.1	109	2	US-09-198-452A-11	Sequence 11, Appl
691	51.5	11.2	307	2	US-10-006-041A-95	Sequence 95, Appl	764	51	11.1	109	2	US-09-438-185A-2	Sequence 2, Appl
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694	51.5	11.2	307	3	US-10-011-795B-95	Sequence 95, Appl	767	51	11.1	205	2	US-09-605-703B-1998	Sequence 1998, Ap
695	51.5	11.2	307	3	US-10-015-386A-95	Sequence 95, Appl	768	51	11.1	211	2	US-09-248-796A-20685	Sequence 20685, A
696	51.5	11.2	307	3	US-10-012-121A-95	Sequence 95, Appl	769	51	11.1	214	1	US-08-277-231A-14	Sequence 14, Appl
697	51.5	11.2	307	3	US-10-006-485A-95	Sequence 95, Appl	770	51	11.1	214	1	US-08-473-750-3	Sequence 3, Appl
698	51.5	11.2	307	3	US-10-006-746A-95	Sequence 95, Appl	771	51	11.1	214	1	US-08-477-326-3	Sequence 3, Appl
699	51.5	11.2	307	3	US-10-012-752A-95	Sequence 95, Appl	772	51	11.1	217	1	US-08-277-231A-12	Sequence 12, Appl
700	51.5	11.2	307	3	US-10-017-253A-95	Sequence 95, Appl	773	51	11.1	217	1	US-08-473-750-1	Sequence 1, Appl
701	51.5	11.2	307	3	US-10-015-519A-95	Sequence 95, Appl	774	51	11.1	217	1	US-08-473-750-5	Sequence 5, Appl
702	51.5	11.2	307	3	US-10-015-715A-95	Sequence 95, Appl	775	51	11.1	217	1	US-08-473-326-1	Sequence 1, Appl
703	51.5	11.2	307	3	US-10-007-236A-95	Sequence 95, Appl	776	51	11.1	217	1	US-08-477-326-5	Sequence 5, Appl
704	51.5	11.2	319	2	US-08-581-148C-12	Sequence 12, Appl	777	51	11.1	217	1	US-08-477-326-5	Sequence 5, Appl
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706	51.5	11.2	334	5	PCT-US93-08528-73	Sequence 73, Appl	779	51	11.1	230	2	US-09-328-352-7370	Sequence 7370, Ap
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709	51.5	11.2	369	2	US-08-880-865-2	Sequence 2, Appl	782	51	11.1	320	2	US-09-902-540-12563	Sequence 12563, A
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712	51.5	11.2	381	1	US-08-467-948A-28	Sequence 28, Appl	785	51	11.1	326	2	US-09-489-039A-11901	Sequence 11901, A
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717	51.5	11.2	382	5	PCT-US96-10618-4	Sequence 4, Appl	790	51	11.1	346	2	US-09-198-452A-60	Sequence 60, Appl
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719	51.5	11.2	382	2	US-09-262-477-2	Sequence 2, Appl	792	51	11.1	361	1	US-09-902-540-15411	Sequence 15411, A
720	51.5	11.2	382	2	US-09-169-205D-21	Sequence 21, Appl	793	51	11.1	361	1	US-08-390-162-4	Sequence 4, Appl
721	51.5	11.2	383	1	US-08-196-989B-4	Sequence 4, Appl	794	51	11.1	361	1	US-08-685-945B-4	Sequence 4, Appl
722	51.5	11.2	383	1	US-08-760-936-4	Sequence 4, Appl	795	51	11.1	365	1	US-08-390-162-2	Sequence 2, Appl
723	51.5	11.2	383	2	US-09-225-024-4	Sequence 4, Appl	796	51	11.1	365	1	US-08-685-945B-2	Sequence 2, Appl
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727	51.5	11.2	390	1	US-08-416-756A-5	Sequence 5, Appl	800	51	11.1	383	2	US-08-530-862B-7	Sequence 7, Appl
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729	51.5	11.2	407	2	US-08-753-007A-6	Sequence 6, Appl	802	51	11.1	430	2	US-09-885-189-7	Sequence 12, Appl
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733	51.5	11.2	495	2	US-09-270-767-44726	Sequence 44726, A	806	51	11.1	475	2	US-09-489-039A-8862	Sequence 8862, Ap
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738	51.5	11.2	549	2	US-09-862-027-32	Sequence 32, Appl	811	51	11.1	584	2	US-09-107-532A-4564	Sequence 4564, Ap
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752	51.5	11.2	1204	2	US-10-094-749-2542	Sequence 2542, Ap	825	51	11.1	967	2	US-10-099-322-75	Sequence 75, Appl
753	51.5	11.2	1451	1	US-08-308-872B-4	Sequence 4, Appl	826	51	11.1	967	2	US-10-044-564-14	Sequence 14, Appl
754	51.5	11.2	1451	2	US-08-392-459-32	Sequence 32, Appl	827	51	11.1	967	2	US-10-044-564-74	Sequence 74, Appl
755	51.5	11.2	1454	2	US-09-854-799-32	Sequence 32, Appl	828	51	11.1	967	2	US-10-044-564-75	Sequence 75, Appl
756	51.5	11.2	1454	5	PCT-US91-08535-32	Sequence 32, Appl	829	51	11.1	1049	2	US-09-854-845-2	Sequence 2, Appl

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539	52.5	11.4	410	2	US-09-189-627A-11	Sequence 11, Appl	612	52	11.3	310	3	US-09-721-047A-4	Sequence 4, Appli
540	52.5	11.4	410	2	US-09-710-861-11	Sequence 11, Appl	613	52	11.3	312	2	US-09-543-681A-6689	Sequence 6689, Ap
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542	52.5	11.4	448	2	US-09-328-532-5807	Sequence 5807, Ap	615	52	11.3	350	2	US-09-543-681A-4618	Sequence 4618, Ap
543	52.5	11.4	468	2	US-09-602-787A-612	Sequence 612, App	616	52	11.3	371	2	US-09-949-016-8635	Sequence 8635, Ap
544	52.5	11.4	483	2	US-09-949-016-7773	Sequence 7773, Ap	617	52	11.3	380	2	US-08-888-429A-30	Sequence 30, Appl
545	52.5	11.4	523	2	US-09-538-092-571	Sequence 571, App	618	52	11.3	380	2	US-09-593-653-30	Sequence 30, Appl
546	52.5	11.4	525	2	US-08-888-949-16	Sequence 16, Appl	619	52	11.3	387	2	US-09-252-991A-22112	Sequence 22112, A
547	52.5	11.4	525	2	US-08-888-950-16	Sequence 16, Appl	620	52	11.3	389	2	US-08-888-429A-20	Sequence 20, Appl
548	52.5	11.4	525	2	US-09-262-758-16	Sequence 16, Appl	621	52	11.3	389	2	US-09-593-653-20	Sequence 20, Appl
549	52.5	11.4	525	2	US-09-885-876-16	Sequence 16, Appl	622	52	11.3	415	2	US-09-543-681A-6292	Sequence 6292, Ap
550	52.5	11.4	525	2	US-09-885-901-16	Sequence 16, Appl	623	52	11.3	419	2	US-08-888-429A-28	Sequence 28, Appl
551	52.5	11.4	525	2	US-09-731-393-16	Sequence 16, Appl	624	52	11.3	419	2	US-09-446-754-6	Sequence 6, Appli
552	52.5	11.4	550	2	US-09-120-365-1	Sequence 1, Appli	625	52	11.3	419	2	US-09-208-166-2	Sequence 2, Appli
553	52.5	11.4	550	2	US-09-515-039-1	Sequence 1, Appli	626	52	11.3	419	2	US-09-208-166-5	Sequence 5, Appli
554	52.5	11.4	551	3	US-09-622-964A-29	Sequence 29, Appl	627	52	11.3	419	2	US-09-593-653-28	Sequence 28, Appl
555	52.5	11.4	609	2	US-09-107-532A-5110	Sequence 5110, Ap	628	52	11.3	420	1	US-08-864-804-1	Sequence 1, Appli
556	52.5	11.4	693	2	US-09-949-016-9666	Sequence 9666, Ap	629	52	11.3	433	2	US-09-949-016-7636	Sequence 7636, Ap
557	52.5	11.4	706	2	US-09-252-991A-25730	Sequence 25730, A	630	52	11.3	435	2	US-09-446-754-2	Sequence 2, Appli
558	52.5	11.4	763	2	US-10-104-047-2766	Sequence 2766, Ap	631	52	11.3	453	2	US-08-888-429A-32	Sequence 32, Appl
559	52.5	11.4	763	3	US-09-502-698-88	Sequence 88, Appl	632	52	11.3	453	2	US-09-593-653-32	Sequence 32, Appl
560	52.5	11.4	800	2	US-09-489-039A-10358	Sequence 10358, A	633	52	11.3	468	2	US-09-446-754-4	Sequence 4, Appli
561	52.5	11.4	801	2	US-09-543-681A-7561	Sequence 7561, Ap	634	52	11.3	468	2	US-09-446-754-10	Sequence 10, Appl
562	52.5	11.4	969	2	US-09-321-987B-5	Sequence 5, Appli	635	52	11.3	475	2	US-09-949-016-11570	Sequence 11570, A
563	52.5	11.4	1000	2	US-09-352-159-25	Sequence 25, Appl	636	52	11.3	482	2	US-09-489-039A-9909	Sequence 9909, Ap
564	52.5	11.4	1000	2	US-09-352-168-25	Sequence 25, Appl	637	52	11.3	521	2	US-08-669-656A-4	Sequence 4, Appli
565	52.5	11.4	1000	2	US-09-771-045B-25	Sequence 25, Appl	638	52	11.3	596	2	US-09-134-001C-3363	Sequence 3363, Ap
566	52.5	11.4	1000	2	US-09-770-564A-25	Sequence 25, Appl	639	52	11.3	628	2	US-09-602-787A-550	Sequence 550, App
567	52.5	11.4	1000	2	US-09-658-835C-25	Sequence 25, Appl	640	52	11.3	628	2	US-09-602-787A-666	Sequence 666, App
568	52.5	11.4	1000	2	US-10-624-619A-25	Sequence 25, Appl	641	52	11.3	736	2	US-09-252-991A-19048	Sequence 19048, A
569	52.5	11.4	1005	3	US-09-502-698-2	Sequence 2, Appli	642	52	11.3	1194	2	US-09-949-016-9803	Sequence 9803, Ap
570	52.5	11.4	1101	2	US-08-331-625A-52	Sequence 52, Appl	643	52	11.3	1195	2	US-09-949-016-6535	Sequence 6535, Ap
571	52.5	11.4	1101	2	US-08-331-625A-54	Sequence 54, Appl	644	52	11.3	1666	2	US-09-949-016-8322	Sequence 8322, Ap
572	52.5	11.4	1101	2	US-09-494-151-52	Sequence 52, Appl	645	52	11.3	1956	2	US-08-843-417-2	Sequence 2, Appli
573	52.5	11.4	1101	2	US-09-494-151-54	Sequence 54, Appl	646	52	11.3	1957	2	US-09-527-013-2	Sequence 2, Appli
574	52.5	11.4	1101	2	US-09-972-484-52	Sequence 52, Appl	647	52	11.3	1957	2	US-08-669-656A-2	Sequence 2, Appli
575	52.5	11.4	1101	2	US-09-972-484-54	Sequence 54, Appl	648	52	11.3	1957	2	US-08-669-656A-8	Sequence 8, Appli
576	52.5	11.4	1205	2	US-09-491-522-11	Sequence 11, Appl	649	52	11.3	2057	2	US-08-499-203-2	Sequence 2, Appli
577	52.5	11.4	1279	2	US-09-489-039A-13602	Sequence 13602, A	650	52	11.3	2132	2	US-08-669-656A-6	Sequence 6, Appli
578	52.5	11.4	1373	3	US-09-602-698-1	Sequence 1, Appli	651	51.5	11.2	123	1	US-09-513-999C-7866	Sequence 7866, Ap
579	52.5	11.4	1452	2	US-08-331-625A-2	Sequence 2, Appli	652	51.5	11.2	123	1	US-08-180-209B-19	Sequence 19, Appl
580	52.5	11.4	1452	2	US-09-494-151-2	Sequence 2, Appli	653	51.5	11.2	123	1	US-08-385-745-19	Sequence 19, Appl
581	52.5	11.4	1452	2	US-09-972-484-2	Sequence 2, Appli	654	51.5	11.2	123	2	US-08-485-388-19	Sequence 19, Appl
582	52.5	11.4	1452	5	PCT-US93-04384-18	Sequence 18, Appl	655	51.5	11.2	123	2	US-08-485-388-19	Sequence 19, Appl
583	52.5	11.4	1452	5	PCT-US93-04692-2	Sequence 2, Appli	656	51.5	11.2	123	2	US-08-478-853-19	Sequence 19, Appl
584	52.5	11.4	1453	1	US-08-308-872B-6	Sequence 6, Appli	657	51.5	11.2	123	2	US-09-166-205B-19	Sequence 19, Appl
585	52.5	11.4	2000	3	US-09-502-698-82	Sequence 82, Appl	658	51.5	11.2	134	2	PCT-US94-02629-19	Sequence 19, Appl
586	52.5	11.4	2037	2	US-09-306-998-3	Sequence 3, Appli	659	51.5	11.2	185	2	US-09-605-703B-1756	Sequence 1756, Ap
587	52.5	11.4	2046	2	US-09-949-016-9365	Sequence 9365, Ap	660	51.5	11.2	185	2	US-09-252-991A-20175	Sequence 20175, A
588	52.5	11.4	2070	3	US-09-502-698-83	Sequence 83, Appl	661	51.5	11.2	187	2	US-09-949-016-9179	Sequence 9179, Ap
589	52	11.3	87	2	US-09-252-991A-17552	Sequence 17552, A	662	51.5	11.2	211	2	US-09-130-491-4	Sequence 4, Appli
590	52	11.3	105	2	US-09-288-143-209	Sequence 209, App	663	51.5	11.2	211	2	US-09-603-552-12	Sequence 12, Appl
591	52	11.3	105	3	US-08-984-429-209	Sequence 209, App	664	51.5	11.2	211	2	US-09-886-683A-4	Sequence 4, Appli
592	52	11.3	127	2	US-09-328-352-4209	Sequence 4209, App	665	51.5	11.2	211	2	US-09-949-016-6992	Sequence 6992, Ap
593	52	11.3	132	2	US-09-454-279-6	Sequence 6, Appli	666	51.5	11.2	211	2	US-09-999-833A-270	Sequence 270, App
594	52	11.3	136	2	US-09-270-767-39814	Sequence 39814, A	667	51.5	11.2	211	2	US-10-020-445A-270	Sequence 270, App
595	52	11.3	136	2	US-09-270-767-55031	Sequence 55031, A	668	51.5	11.2	211	2	US-09-978-189-270	Sequence 270, App
596	52	11.3	160	2	US-09-583-110-5206	Sequence 5206, Ap	669	51.5	11.2	211	2	US-10-017-085A-270	Sequence 270, App
597	52	11.3	161	2	US-09-107-433-3565	Sequence 3565, Ap	670	51.5	11.2	211	3	US-10-145-129A-270	Sequence 270, App
598	52	11.3	175	2	US-09-270-767-46710	Sequence 46710, A	671	51.5	11.2	211	3	US-10-013-929A-270	Sequence 270, App
599	52	11.3	216	2	US-09-107-532A-3711	Sequence 3711, Ap	672	51.5	11.2	211	3	US-10-013-917A-270	Sequence 270, App
600	52	11.3	218	2	US-10-094-749-2232	Sequence 2232, Ap	673	51.5	11.2	212	1	US-08-461-859-35	Sequence 35, Appl
601	52	11.3	231	2	US-09-303-518D-432	Sequence 432, App	674	51.5	11.2	212	2	US-09-917-254-62	Sequence 62, Appl
602	52	11.3	260	2	US-09-025-059-3	Sequence 3, Appli	675	51.5	11.2	224	2	US-08-871-572B-13	Sequence 13, Appl
603	52	11.3	260	2	US-08-888-429A-26	Sequence 26, Appl	676	51.5	11.2	240	2	US-09-252-991A-30410	Sequence 30410, A
604	52	11.3	260	2	US-09-593-653-26	Sequence 26, Appl	677	51.5	11.2	241	2	US-10-076-069-4	Sequence 4, Appli
605	52	11.3	260	2	US-09-618-259-8	Sequence 8, Appli	678	51.5	11.2	247	2	US-09-949-016-11579	Sequence 11579, A
606	52	11.3	260	3	US-08-915-659A-10	Sequence 10, Appl	679	51.5	11.2	250	2	US-09-167-717-1	Sequence 1, Appli
607	52	11.3	261	2	US-09-454-279-16	Sequence 16, Appl	680	51.5	11.2	268	2	US-09-818-780-17	Sequence 17, Appl
608	52	11.3	262	2	US-09-303-518D-434	Sequence 434, App	681	51.5	11.2	268	2	US-09-818-780-94	Sequence 94, Appl
609	52	11.3	267	2	US-09-248-796A-17580	Sequence 17580, A	682	51.5	11.2	292	2	US-09-205-258-1116	Sequence 1116, Ap
610	52	11.3	285	3	US-09-721-047A-21	Sequence 21, Appl	683	51.5	11.2	292	2	US-10-004-860-1116	Sequence 1116, Ap

392	54	11.7	447	5	PCT-US94-07280-20	Sequence 20, Appl	465	53	11.5	377	2	US-09-538-032-1199	Sequence 1199, Ap
393	54	11.7	447	5	PCT-US95-01087-20	Sequence 20, Appl	466	53	11.5	407	2	US-09-489-039A-13350	Sequence 13350, A
394	54	11.7	453	1	US-08-188-281B-16	Sequence 16, Appl	467	53	11.5	415	2	US-10-094-749-2139	Sequence 2139, Ap
395	54	11.7	453	1	PCT-US94-07280-16	Sequence 16, Appl	468	53	11.5	454	2	US-09-949-016-10198	Sequence 10198, A
396	54	11.7	453	5	PCT-US95-01087-16	Sequence 16, Appl	469	53	11.5	460	2	US-09-489-039A-13505	Sequence 13505, A
397	54	11.7	478	2	US-09-489-039A-7367	Sequence 7367, Ap	470	53	11.5	469	2	US-09-902-540-12213	Sequence 12213, A
398	54	11.7	490	1	US-08-188-281B-15	Sequence 15, Appl	471	53	11.5	473	2	US-10-094-749-1936	Sequence 1936, Ap
399	54	11.7	490	5	PCT-US94-07280-15	Sequence 15, Appl	472	53	11.5	474	2	US-09-489-039A-10791	Sequence 10791, A
400	54	11.7	490	5	PCT-US95-01087-15	Sequence 15, Appl	473	53	11.5	476	2	US-09-489-039A-12217	Sequence 12217, A
401	54	11.7	493	2	US-09-170-984-2	Sequence 2, Appl	474	53	11.5	482	2	US-09-438-185A-356	Sequence 356, App
402	54	11.7	518	2	US-09-540-236-3648	Sequence 3648, Ap	475	53	11.5	524	2	US-09-549-519-27	Sequence 27, Appl
403	54	11.7	880	2	US-09-538-092-601	Sequence 601, A	476	53	11.5	524	2	US-09-549-519-28	Sequence 28, Appl
404	54	11.7	891	2	US-09-252-991A-28689	Sequence 28689, A	477	53	11.5	563	2	US-09-949-016-8277	Sequence 8277, Ap
405	54	11.7	1036	2	US-09-902-540-14218	Sequence 14218, A	478	53	11.5	574	2	US-09-248-796A-16849	Sequence 16849, A
406	54	11.7	3623	2	US-09-341-461-2	Sequence 2, Appl	479	53	11.5	580	2	US-09-489-039A-8096	Sequence 8096, Ap
407	53.5	11.6	72	2	US-09-188-930-182	Sequence 182, App	480	53	11.5	605	2	US-09-902-540-12393	Sequence 12393, A
408	53.5	11.6	221	2	US-09-464-535-22	Sequence 22, Appl	481	53	11.5	661	2	US-09-540-236-3743	Sequence 3743, Ap
409	53.5	11.6	239	3	US-09-936-271C-71	Sequence 71, Appl	482	53	11.5	678	2	US-09-252-991A-20202	Sequence 20202, A
410	53.5	11.6	244	1	US-08-361-395-1	Sequence 1, Appl	483	53	11.5	686	2	US-09-252-991A-19332	Sequence 19332, A
411	53.5	11.6	244	2	US-09-618-259-11	Sequence 11, Appl	484	53	11.5	792	2	US-09-995-587A-11	Sequence 11, Appl
412	53.5	11.6	244	3	US-09-936-271C-84	Sequence 84, Appl	485	53	11.5	896	2	US-09-585-588-17	Sequence 17, Appl
413	53.5	11.6	272	2	US-09-583-110-3866	Sequence 3866, Ap	486	53	11.5	1016	2	US-10-270-878-17	Sequence 17, Appl
414	53.5	11.6	284	2	US-09-902-540-16417	Sequence 16417, A	487	53	11.5	1070	2	US-09-252-991A-18914	Sequence 18914, A
415	53.5	11.6	302	2	US-09-252-991A-21655	Sequence 21655, A	488	53	11.5	1145	2	US-09-961-403-3	Sequence 3, Appl
416	53.5	11.6	308	2	US-09-489-039A-14278	Sequence 14278, A	489	53	11.5	1146	2	US-09-824-734-2	Sequence 2, Appl
417	53.5	11.6	310	2	US-09-107-433-4601	Sequence 4601, Ap	490	53	11.5	1238	2	US-09-904-065-2	Sequence 2, Appl
418	53.5	11.6	325	2	US-09-949-016-7713	Sequence 7713, Ap	491	53	11.5	1238	2	US-09-904-065-14	Sequence 14, Appl
419	53.5	11.6	359	2	US-08-637-670-37	Sequence 37, Appl	492	53	11.5	1240	1	US-08-680-326-37	Sequence 37, Appl
420	53.5	11.6	382	2	US-09-489-039A-13696	Sequence 13696, A	493	53	11.5	1240	2	US-09-904-065-4	Sequence 4, Appl
421	53.5	11.6	407	2	US-09-710-279-1578	Sequence 1578, Ap	494	53	11.5	1240	2	US-09-904-065-15	Sequence 15, Appl
422	53.5	11.6	410	1	US-08-723-415B-10	Sequence 10, Appl	495	53	11.5	1326	2	US-09-949-016-6806	Sequence 6806, Ap
423	53.5	11.6	410	2	US-09-189-627A-10	Sequence 10, Appl	496	53	11.5	1326	2	US-09-949-016-10448	Sequence 10448, A
424	53.5	11.6	410	2	US-09-710-861-10	Sequence 10, Appl	497	53	11.5	1478	2	US-09-949-016-8315	Sequence 8315, Ap
425	53.5	11.6	417	2	US-09-949-016-8808	Sequence 8808, Ap	498	52.5	11.4	21	2	US-09-962-756-592	Sequence 592, App
426	53.5	11.6	437	2	US-09-350-841A-1591	Sequence 1591, Ap	499	52.5	11.4	71	2	US-09-369-247-79	Sequence 79, Appl
427	53.5	11.6	438	2	US-08-486-099-105	Sequence 105, App	500	52.5	11.4	71	2	US-10-062-548-79	Sequence 79, Appl
428	53.5	11.6	438	2	US-08-360-107A-115	Sequence 115, App	501	52.5	11.4	123	2	US-09-107-532A-4652	Sequence 4652, Ap
429	53.5	11.6	438	2	US-08-484-223B-105	Sequence 105, App	502	52.5	11.4	126	2	US-08-331-625A-9	Sequence 9, Appl
430	53.5	11.6	438	2	US-08-919-597-105	Sequence 105, App	503	52.5	11.4	126	2	US-09-494-151-9	Sequence 9, Appl
431	53.5	11.6	438	2	US-08-475-668A-105	Sequence 105, App	504	52.5	11.4	126	2	US-09-972-484-9	Sequence 9, Appl
432	53.5	11.6	438	2	US-08-485-551A-105	Sequence 105, App	505	52.5	11.4	158	2	US-09-464-535-8	Sequence 8, Appl
433	53.5	11.6	438	2	US-08-471-913A-105	Sequence 105, App	506	52.5	11.4	167	2	US-09-438-185A-132	Sequence 132, App
434	53.5	11.6	438	2	US-08-485-264A-105	Sequence 105, App	507	52.5	11.4	216	2	US-09-464-535-28	Sequence 28, Appl
435	53.5	11.6	438	2	US-08-474-349A-105	Sequence 105, App	508	52.5	11.4	236	2	US-09-270-757-44948	Sequence 44948, A
436	53.5	11.6	438	2	US-08-470-896-105	Sequence 105, App	509	52.5	11.4	251	2	US-08-331-625A-59	Sequence 59, Appl
437	53.5	11.6	438	2	US-08-485-546A-105	Sequence 105, App	510	52.5	11.4	251	2	US-09-494-151-59	Sequence 59, Appl
438	53.5	11.6	438	2	US-08-487-266A-105	Sequence 105, App	511	52.5	11.4	251	2	US-09-972-484-59	Sequence 59, Appl
439	53.5	11.6	438	2	US-08-484-741-105	Sequence 105, App	512	52.5	11.4	384	2	US-08-907-608-6	Sequence 6, Appl
440	53.5	11.6	440	2	US-09-134-001C-3286	Sequence 3286, Ap	513	52.5	11.4	384	2	US-09-354-231B-6	Sequence 6, Appl
441	53.5	11.6	495	2	US-09-275-252A-5	Sequence 5, Appl	514	52.5	11.4	384	2	US-09-354-231B-8	Sequence 8, Appl
442	53.5	11.6	550	1	US-08-279-700-16	Sequence 16, Appl	515	52.5	11.4	384	2	US-09-354-231B-10	Sequence 10, Appl
443	53.5	11.6	550	2	US-09-230-944-18	Sequence 18, Appl	516	52.5	11.4	384	2	US-09-354-231B-12	Sequence 12, Appl
444	53.5	11.6	550	2	US-09-230-944-20	Sequence 20, Appl	517	52.5	11.4	384	2	US-09-133-962A-4	Sequence 4, Appl
445	53.5	11.6	550	2	US-09-873-233A-18	Sequence 18, Appl	518	52.5	11.4	384	2	US-09-128-602B-6	Sequence 6, Appl
446	53.5	11.6	550	2	US-09-873-233A-20	Sequence 20, Appl	519	52.5	11.4	384	2	US-09-128-602B-8	Sequence 8, Appl
447	53.5	11.6	550	2	US-10-149-634-2	Sequence 2, Appl	520	52.5	11.4	384	2	US-09-128-602B-10	Sequence 10, Appl
448	53.5	11.6	898	2	US-10-449-315-11	Sequence 11, Appl	521	52.5	11.4	384	2	US-09-128-602B-12	Sequence 12, Appl
449	53	11.5	68	2	US-09-243-675-3	Sequence 3, Appl	522	52.5	11.4	384	2	US-09-482-887-6	Sequence 6, Appl
450	53	11.5	78	2	US-09-749-637A-228	Sequence 228, App	523	52.5	11.4	384	2	US-09-965-288-6	Sequence 6, Appl
451	53	11.5	165	2	US-10-104-047-2538	Sequence 2538, Ap	524	52.5	11.4	384	2	US-09-995-297-6	Sequence 6, Appl
452	53	11.5	223	2	US-09-605-703B-2326	Sequence 2326, Ap	525	52.5	11.4	384	2	US-09-995-297-8	Sequence 8, Appl
453	53	11.5	225	2	US-09-543-681A-4579	Sequence 4579, Ap	526	52.5	11.4	384	2	US-09-995-297-10	Sequence 10, Appl
454	53	11.5	237	3	US-08-936-271C-66	Sequence 66, Appl	527	52.5	11.4	384	2	US-09-995-297-12	Sequence 12, Appl
455	53	11.5	239	2	US-08-913-014A-2	Sequence 2, Appl	528	52.5	11.4	384	2	US-09-697-379-4	Sequence 4, Appl
456	53	11.5	251	3	US-09-653-285-2	Sequence 2, Appl	529	52.5	11.4	384	2	US-10-116-212A-4	Sequence 4, Appl
457	53	11.5	251	3	US-09-936-271C-67	Sequence 67, Appl	530	52.5	11.4	384	2	US-09-771-904A-6	Sequence 6, Appl
458	53	11.5	299	2	US-09-252-991A-24215	Sequence 24215, A	531	52.5	11.4	384	2	US-09-771-904A-8	Sequence 8, Appl
459	53	11.5	319	2	US-09-134-000C-6061	Sequence 6061, Ap	532	52.5	11.4	384	2	US-09-771-904A-10	Sequence 10, Appl
460	53	11.5	348	2	US-09-134-001C-4857	Sequence 4857, Ap	533	52.5	11.4	384	2	US-09-771-904A-12	Sequence 12, Appl
461	53	11.5	355	2	US-09-902-540-14706	Sequence 14706, A	534	52.5	11.4	396	2	US-09-198-452A-147	Sequence 147, App
462	53	11.5	356	2	US-09-664-840-2	Sequence 2, Appl	535	52.5	11.4	410	1	US-08-723-415B-11	Sequence 11, Appl
463	53	11.5	377	1	US-08-188-277B-4	Sequence 4, Appl	536	52.5	11.4	410	1	US-08-428-131-2	Sequence 2, Appl
464	53	11.5	377	1	US-08-429-964-78	Sequence 78, Appl	537	52.5	11.4	410	1	US-08-602-846-2	Sequence 2, Appl

246	55.5	12.0	559	2	US-08-767-993-15	Sequence 15, Appl	319	54.5	11.8	631	2	US-09-328-352-6860	Sequence 6860, Ap
247	55.5	12.0	687	1	US-08-555-568B-21	Sequence 21, Appl	320	54.5	11.8	752	1	US-08-281-193-2	Sequence 2, Appl
248	55.5	12.0	687	2	US-09-519-223-21	Sequence 21, Appl	321	54.5	11.8	752	1	US-08-422-106-2	Sequence 2, Appl
249	55.5	12.0	687	2	US-09-927-180-21	Sequence 21, Appl	322	54.5	11.8	752	1	US-08-735-716-2	Sequence 2, Appl
250	55.5	12.0	688	1	US-08-555-568B-23	Sequence 23, Appl	323	54.5	11.8	752	1	US-08-555-568B-2	Sequence 2, Appl
251	55.5	12.0	688	2	US-09-519-223-23	Sequence 23, Appl	324	54.5	11.8	752	1	US-09-519-223-2	Sequence 2, Appl
252	55.5	12.0	688	2	US-09-927-180-23	Sequence 23, Appl	325	54.5	11.8	752	1	US-09-927-180-2	Sequence 2, Appl
253	55.5	12.0	688	2	US-09-949-016-10948	Sequence 10948, A	326	54.5	11.8	752	5	PCT-US95-08069-2	Sequence 2, Appl
254	55.5	12.0	887	2	US-09-077-940A-2	Sequence 2, Appl	327	54.5	11.8	765	2	US-09-949-016-7844	Sequence 7844, Ap
255	55.5	12.0	888	2	US-09-077-940A-4	Sequence 4, Appl	328	54.5	11.8	780	2	US-09-902-540-10063	Sequence 10063, A
256	55.5	12.0	888	2	US-10-036-041-35	Sequence 35, Appl	329	54.5	11.8	781	1	US-08-280-690-2	Sequence 2, Appl
257	55.5	12.0	968	2	US-09-228-986-76	Sequence 76, Appl	330	54.5	11.8	895	1	US-08-123-161A-8	Sequence 8, Appl
258	55.5	12.0	968	2	US-10-101-464A-76	Sequence 76, Appl	331	54.5	11.8	895	1	US-08-483-278-8	Sequence 8, Appl
259	55	11.9	124	2	US-09-270-767-33906	Sequence 33906, A	332	54.5	11.8	895	2	US-09-949-016-6490	Sequence 6490, Ap
260	55	11.9	124	2	US-09-270-767-49123	Sequence 49123, A	333	54.5	11.8	920	2	US-09-949-016-7178	Sequence 7178, Ap
261	55	11.9	205	2	US-09-248-796A-15224	Sequence 15224, A	334	54.5	11.8	1021	2	US-10-094-749-3055	Sequence 3055, Ap
262	55	11.9	232	1	US-08-456-670B-39	Sequence 39, Appl	335	54	11.7	135	1	US-08-188-281B-6	Sequence 6, Appl
263	55	11.9	232	2	US-09-372-036-39	Sequence 39, Appl	336	54	11.7	135	5	PCT-US94-07280-6	Sequence 6, Appl
264	55	11.9	359	2	US-09-248-796A-18202	Sequence 18202, A	337	54	11.7	135	5	PCT-US95-01087-6	Sequence 6, Appl
265	55	11.9	376	2	US-09-103-331-42	Sequence 42, Appl	338	54	11.7	172	1	US-08-188-281B-5	Sequence 5, Appl
266	55	11.9	376	2	US-09-631-594-51	Sequence 51, Appl	339	54	11.7	172	5	PCT-US94-07280-5	Sequence 5, Appl
267	55	11.9	381	2	US-09-248-796A-19630	Sequence 19630, A	340	54	11.7	172	5	PCT-US95-01087-5	Sequence 5, Appl
268	55	11.9	404	2	US-09-538-092-50	Sequence 50, Appl	341	54	11.7	178	2	US-09-936-588-42	Sequence 42, Appl
269	55	11.9	406	2	US-09-252-991A-20630	Sequence 20630, A	342	54	11.7	221	1	US-08-188-281B-2	Sequence 2, Appl
270	55	11.9	459	2	US-08-311-731A-47	Sequence 47, Appl	343	54	11.7	221	5	PCT-US94-07280-2	Sequence 2, Appl
271	55	11.9	478	1	US-08-456-670B-40	Sequence 40, Appl	344	54	11.7	221	5	PCT-US95-01087-2	Sequence 2, Appl
272	55	11.9	478	2	US-09-372-036-40	Sequence 40, Appl	345	54	11.7	241	2	US-09-005-298-46	Sequence 46, Appl
273	55	11.9	484	1	US-08-127-499A-26	Sequence 26, Appl	346	54	11.7	241	2	US-08-768-619-46	Sequence 46, Appl
274	55	11.9	484	1	US-08-482-847-26	Sequence 26, Appl	347	54	11.7	346	2	US-09-702-705-329	Sequence 329, App
275	55	11.9	512	1	US-08-173-508-4	Sequence 4, Appl	348	54	11.7	346	2	US-09-736-457-329	Sequence 329, App
276	55	11.9	512	1	US-08-265-310-4	Sequence 4, Appl	349	54	11.7	346	2	US-09-614-124B-329	Sequence 329, App
277	55	11.9	512	2	US-08-351-742-4	Sequence 4, Appl	350	54	11.7	346	2	US-09-671-325-339	Sequence 329, App
278	55	11.9	533	2	US-09-549-519-32	Sequence 32, Appl	351	54	11.7	346	2	US-09-589-184-329	Sequence 329, App
279	55	11.9	598	2	US-09-252-991A-25875	Sequence 25875, A	352	54	11.7	346	2	US-09-658-824-329	Sequence 329, App
280	55	11.9	666	1	US-08-083-590A-17	Sequence 17, Appl	353	54	11.7	346	2	US-10-017-754-329	Sequence 329, App
281	55	11.9	666	2	US-08-346-128-36	Sequence 36, Appl	354	54	11.7	346	2	US-09-651-563-329	Sequence 329, App
282	55	11.9	666	2	US-08-532-384-17	Sequence 17, Appl	355	54	11.7	346	2	US-09-519-642-329	Sequence 329, App
283	55	11.9	1481	1	US-08-616-844-40	Sequence 40, Appl	356	54	11.7	346	2	US-10-099-322-24	Sequence 24, Appl
284	55	11.9	1481	1	US-08-599-654-40	Sequence 40, Appl	357	54	11.7	346	2	US-10-099-322-96	Sequence 96, Appl
285	55	11.9	1481	2	US-08-944-868A-40	Sequence 40, Appl	358	54	11.7	346	2	US-10-099-322-97	Sequence 97, Appl
286	55	11.9	1481	2	US-08-944-423A-40	Sequence 40, Appl	359	54	11.7	346	2	US-10-044-564-24	Sequence 24, Appl
287	55	11.9	1481	2	US-08-944-496-40	Sequence 40, Appl	360	54	11.7	346	2	US-10-044-564-96	Sequence 96, Appl
288	54.5	11.8	102	2	US-09-540-236-2816	Sequence 2816, Ap	361	54	11.7	346	2	US-10-044-564-97	Sequence 97, Appl
289	54.5	11.8	139	2	US-09-270-767-32364	Sequence 32364, A	362	54	11.7	348	2	US-10-099-322-69	Sequence 69, Appl
290	54.5	11.8	139	2	US-09-270-767-47581	Sequence 47581, A	363	54	11.7	348	2	US-10-099-322-98	Sequence 98, Appl
291	54.5	11.8	221	2	US-09-270-767-31937	Sequence 31937, A	364	54	11.7	348	2	US-10-099-322-99	Sequence 99, Appl
292	54.5	11.8	221	2	US-09-270-767-47154	Sequence 47154, A	365	54	11.7	348	2	US-10-044-564-69	Sequence 69, Appl
293	54.5	11.8	240	2	US-09-502-540-11028	Sequence 11028, A	366	54	11.7	348	2	US-10-044-564-98	Sequence 98, Appl
294	54.5	11.8	240	2	US-08-975-811-59	Sequence 59, Appl	367	54	11.7	348	2	US-10-044-564-99	Sequence 99, Appl
295	54.5	11.8	267	2	US-09-634-238-278	Sequence 278, App	368	54	11.7	377	1	US-08-188-281B-17	Sequence 17, Appl
296	54.5	11.8	384	1	US-08-675-650B-4	Sequence 4, Appl	369	54	11.7	377	5	PCT-US94-07280-17	Sequence 17, Appl
297	54.5	11.8	384	1	US-08-675-650B-6	Sequence 6, Appl	370	54	11.7	377	5	PCT-US95-01087-17	Sequence 17, Appl
298	54.5	11.8	384	2	US-08-907-608-2	Sequence 2, Appl	371	54	11.7	395	2	US-09-540-236-2520	Sequence 2520, Ap
299	54.5	11.8	384	2	US-08-907-608-4	Sequence 4, Appl	372	54	11.7	397	1	US-08-188-281B-11	Sequence 11, Appl
300	54.5	11.8	384	2	US-09-059-769-10	Sequence 10, Appl	373	54	11.7	397	5	PCT-US94-07280-11	Sequence 11, Appl
301	54.5	11.8	384	2	US-09-354-231B-2	Sequence 2, Appl	374	54	11.7	397	5	PCT-US95-01087-11	Sequence 11, Appl
302	54.5	11.8	384	2	US-09-354-231B-4	Sequence 4, Appl	375	54	11.7	410	1	US-08-188-281B-18	Sequence 18, Appl
303	54.5	11.8	384	2	US-09-128-602B-2	Sequence 2, Appl	376	54	11.7	410	5	PCT-US94-07280-18	Sequence 18, Appl
304	54.5	11.8	384	2	US-09-128-602B-4	Sequence 4, Appl	377	54	11.7	410	5	PCT-US95-01087-18	Sequence 18, Appl
305	54.5	11.8	384	2	US-09-482-287-2	Sequence 2, Appl	378	54	11.7	412	1	US-09-489-039A-9118	Sequence 9118, Ap
306	54.5	11.8	384	2	US-09-482-287-4	Sequence 4, Appl	379	54	11.7	417	1	US-08-188-281B-19	Sequence 19, Appl
307	54.5	11.8	384	2	US-09-482-287-2	Sequence 2, Appl	380	54	11.7	417	5	PCT-US94-07280-19	Sequence 19, Appl
308	54.5	11.8	384	2	US-09-482-287-4	Sequence 4, Appl	381	54	11.7	417	5	PCT-US95-01087-19	Sequence 19, Appl
309	54.5	11.8	384	2	US-09-995-297-2	Sequence 2, Appl	382	54	11.7	434	1	US-08-188-281B-10	Sequence 10, Appl
310	54.5	11.8	384	2	US-09-995-297-4	Sequence 4, Appl	383	54	11.7	434	5	PCT-US94-07280-10	Sequence 10, Appl
311	54.5	11.8	384	2	US-09-771-904A-2	Sequence 2, Appl	384	54	11.7	434	5	PCT-US95-01087-10	Sequence 10, Appl
312	54.5	11.8	384	2	US-09-771-904A-4	Sequence 4, Appl	385	54	11.7	441	1	US-08-188-281B-21	Sequence 21, Appl
313	54.5	11.8	426	2	US-09-902-540-12322	Sequence 12322, A	386	54	11.7	441	5	PCT-US94-07280-21	Sequence 21, Appl
314	54.5	11.8	446	2	US-09-543-681A-5864	Sequence 5864, Ap	387	54	11.7	441	5	PCT-US95-01087-21	Sequence 21, Appl
315	54.5	11.8	477	2	US-09-489-039A-10570	Sequence 10570, A	388	54	11.7	443	2	US-09-461-325-147	Sequence 147, App
316	54.5	11.8	481	2	US-09-724-623-77	Sequence 77, Appl	389	54	11.7	443	2	US-10-012-542-147	Sequence 147, App
317	54.5	11.8	481	3	US-10-288-930-77	Sequence 77, Appl	390	54	11.7	443	2	US-10-115-123-147	Sequence 147, App
318	54.5	11.8	613	2	US-09-328-352-7962	Sequence 7962, Ap	391	54	11.7	447	1	US-08-188-281B-20	Sequence 20, Appl

100	60	13.0	234	2	US-09-248-796A-17625	Sequence 17625, A	173	56.5	12.3	233	2	US-08-818-111-77	Sequence 77, Appl
101	60	13.0	337	2	US-08-930-830B-2	Sequence 2, Appli	174	56.5	12.3	233	2	US-09-056-556-76	Sequence 76, Appl
102	60	13.0	402	2	US-08-930-830B-5	Sequence 5, Appli	175	56.5	12.3	233	2	US-09-072-596-77	Sequence 77, Appl
103	60	13.0	344	2	US-09-949-016-7352	Sequence 7352, Ap	176	56.5	12.3	233	2	US-09-072-967-76	Sequence 76, Appl
104	60	13.0	426	2	US-09-252-991A-27522	Sequence 27522, A	177	56.5	12.3	233	2	US-10-193-002-77	Sequence 77, Appl
105	60	13.0	497	2	US-09-718-693A-1	Sequence 1, Appli	178	56.5	12.3	233	2	US-10-084-843-76	Sequence 76, Appl
106	59	12.8	83	2	US-09-227-357-652	Sequence 652, App	179	56.5	12.3	260	2	US-09-008-271A-7	Sequence 7, Appli
107	59	12.8	83	2	US-09-973-278-370	Sequence 370, App	180	56.5	12.3	260	2	US-09-968-415-7	Sequence 7, Appli
108	59	12.8	430	2	US-09-133-000C-4819	Sequence 4819, Ap	181	56.5	12.3	385	1	US-08-416-756A-3	Sequence 3, Appli
109	59	12.8	539	1	US-08-464-340A-13	Sequence 13, Appl	182	56.5	12.3	385	2	US-08-880-865-3	Sequence 3, Appli
110	59	12.8	806	2	US-09-833-466-13	Sequence 13, Appl	183	56.5	12.3	419	2	US-08-115-753-2	Sequence 2, Appli
111	59	12.8	854	2	US-09-833-466-12	Sequence 12, Appl	184	56.5	12.3	419	2	US-08-115-753-33	Sequence 33, Appl
112	59	12.8	858	2	US-09-275-252A-6	Sequence 6, Appli	185	56.5	12.3	601	2	US-09-949-016-9977	Sequence 9977, Ap
113	58.5	12.7	142	2	US-09-543-681A-5222	Sequence 5222, Ap	186	56.5	12.3	626	2	US-09-957-187-83	Sequence 83, Appl
114	58.5	12.7	200	2	US-09-252-991A-27855	Sequence 27855, A	187	56.5	12.3	630	2	US-09-520-781-30	Sequence 30, Appl
115	58.5	12.7	243	2	US-09-107-532A-4908	Sequence 4908, Ap	188	56.5	12.3	630	2	US-09-957-187-30	Sequence 30, Appl
116	58.5	12.7	260	2	US-09-070-526-2	Sequence 2, Appli	189	56.5	12.3	630	2	US-09-991-053-30	Sequence 30, Appl
117	58.5	12.7	260	2	US-09-618-259-7	Sequence 7, Appli	190	56.5	12.3	630	2	US-10-101-464A-940	Sequence 940, App
118	58.5	12.7	260	2	US-09-999-833A-395	Sequence 395, App	191	56.5	12.3	757	2	US-09-949-016-7121	Sequence 7121, Ap
119	58.5	12.7	260	2	US-10-020-445A-395	Sequence 395, App	192	56.5	12.3	852	1	US-08-190-802A-59	Sequence 59, Appl
120	58.5	12.7	260	2	US-09-978-189-395	Sequence 395, App	193	56.5	12.3	852	1	US-08-190-802A-67	Sequence 67, Appl
121	58.5	12.7	260	2	US-10-017-085A-395	Sequence 395, App	194	56.5	12.3	852	2	US-08-477-346-67	Sequence 67, Appl
122	58.5	12.7	260	3	US-08-915-659A-7	Sequence 7, Appli	195	56.5	12.3	852	2	US-08-477-346-67	Sequence 67, Appl
123	58.5	12.7	260	3	US-10-145-129A-395	Sequence 395, App	196	56.5	12.3	852	2	US-08-473-089-59	Sequence 59, Appl
124	58.5	12.7	260	3	US-10-013-929A-395	Sequence 395, App	197	56.5	12.3	852	2	US-08-473-089-67	Sequence 67, Appl
125	58.5	12.7	260	3	US-09-936-271C-83	Sequence 83, Appl	198	56.5	12.3	852	2	US-08-487-072A-59	Sequence 59, Appl
126	58.5	12.7	260	3	US-10-013-917A-395	Sequence 395, App	199	56.5	12.3	852	2	US-08-487-072A-67	Sequence 67, Appl
127	58.5	12.7	275	3	US-09-936-271C-72	Sequence 72, Appl	200	56.5	12.3	884	2	US-09-520-781-6	Sequence 6, Appli
128	58.5	12.7	383	1	US-08-314-596-41	Sequence 41, Appl	201	56.5	12.3	884	2	US-09-957-187-6	Sequence 6, Appli
129	58.5	12.7	383	1	US-08-320-982-41	Sequence 41, Appl	202	56.5	12.3	884	2	US-09-991-053-6	Sequence 6, Appli
130	58.5	12.7	383	2	US-08-819-037-41	Sequence 41, Appl	203	56.5	12.3	939	2	US-09-520-781-4	Sequence 4, Appli
131	58.5	12.7	383	2	US-08-530-862B-6	Sequence 6, Appli	204	56.5	12.3	939	2	US-09-957-187-4	Sequence 4, Appli
132	58.5	12.7	383	2	US-08-597-313D-6	Sequence 6, Appli	205	56.5	12.3	939	2	US-09-991-053-4	Sequence 4, Appli
133	58.5	12.7	383	2	US-09-059-769-9	Sequence 9, Appli	206	56.5	12.3	1030	2	US-09-856-681A-2	Sequence 2, Appli
134	58.5	12.7	383	2	US-09-161-994A-14	Sequence 14, Appl	207	56.5	12.3	1030	2	US-09-856-681A-7	Sequence 7, Appli
135	58.5	12.7	383	2	US-09-133-962A-2	Sequence 2, Appli	208	56.5	12.3	1047	2	US-09-957-187-85	Sequence 85, Appl
136	58.5	12.7	383	2	US-09-045-940-41	Sequence 41, Appl	209	56	12.1	199	2	US-09-543-681A-5720	Sequence 5720, Ap
137	58.5	12.7	383	2	US-09-763-331-4	Sequence 4, Appli	210	56	12.1	202	2	US-09-489-039A-8619	Sequence 8619, Ap
138	58.5	12.7	383	2	US-09-697-373-2	Sequence 2, Appli	211	56	12.1	216	2	US-09-540-236-3467	Sequence 3467, Ap
139	58.5	12.7	383	2	US-10-116-212A-2	Sequence 2, Appli	212	56	12.1	319	2	US-09-540-236-2071	Sequence 2071, Ap
140	58.5	12.7	383	2	US-09-885-189-6	Sequence 6, Appli	213	56	12.1	593	2	US-09-949-016-10355	Sequence 10355, A
141	58.5	12.7	383	2	US-09-837-751-32	Sequence 32, Appl	214	56	12.1	605	2	US-09-252-991A-24349	Sequence 24349, A
142	58.5	12.7	518	2	US-09-902-540-14949	Sequence 14949, A	215	56	12.1	1058	2	US-09-949-016-11457	Sequence 11457, A
143	58.5	12.7	1058	2	US-09-489-039A-11177	Sequence 11177, A	216	56	12.1	1384	2	US-08-826-114-2	Sequence 2, Appli
144	58	12.6	228	2	US-09-489-039A-10271	Sequence 10271, A	217	56	12.1	1384	2	US-09-949-016-6395	Sequence 6395, Ap
145	58	12.6	427	2	US-09-902-540-14326	Sequence 14326, A	218	56	12.1	1633	2	US-09-902-540-12892	Sequence 12892, A
146	58	12.6	681	2	US-10-104-047-3586	Sequence 3586, Ap	219	56	12.1	1805	2	US-09-949-016-8246	Sequence 8246, Ap
147	57.5	12.5	27	2	US-09-962-756-1644	Sequence 1644, Ap	220	55.5	12.0	175	2	US-09-252-991A-32945	Sequence 32945, A
148	57.5	12.5	352	2	US-09-252-991A-17455	Sequence 17455, A	221	55.5	12.0	248	1	US-08-313-553-3	Sequence 3, Appli
149	57.5	12.5	471	2	US-09-252-991A-17897	Sequence 17897, A	222	55.5	12.0	248	1	US-08-303-651-2	Sequence 2, Appli
150	57.5	12.5	471	2	US-09-328-352-5145	Sequence 5145, Ap	223	55.5	12.0	248	1	US-08-767-993-3	Sequence 3, Appli
151	57.5	12.5	499	2	US-09-902-540-12205	Sequence 12205, A	224	55.5	12.0	262	1	US-08-313-553-2	Sequence 2, Appli
152	57.5	12.5	528	1	US-08-527-152-2	Sequence 2, Appli	225	55.5	12.0	262	1	US-08-767-993-2	Sequence 2, Appli
153	57.5	12.5	775	2	US-09-252-991A-28461	Sequence 28461, A	226	55.5	12.0	292	1	US-08-555-568B-19	Sequence 19, Appl
154	57.5	12.5	1107	2	US-09-489-039A-8890	Sequence 8890, Ap	227	55.5	12.0	292	2	US-09-519-223-19	Sequence 19, Appl
155	57	12.4	185	2	US-10-018-924-6	Sequence 6, Appli	228	55.5	12.0	292	2	US-09-927-180-19	Sequence 19, Appl
156	57	12.4	647	2	US-09-543-681A-5240	Sequence 5240, Ap	229	55.5	12.0	348	2	US-09-248-796A-19460	Sequence 19460, A
157	56.5	12.3	89	1	US-07-939-501A-2	Sequence 2, Appli	230	55.5	12.0	384	1	US-08-675-650B-8	Sequence 2, Appli
158	56.5	12.3	89	1	US-07-966-187-5	Sequence 5, Appli	231	55.5	12.0	384	2	US-09-354-231B-14	Sequence 14, Appl
159	56.5	12.3	89	1	US-08-371-121-4	Sequence 4, Appli	232	55.5	12.0	384	2	US-09-354-231B-16	Sequence 16, Appl
160	56.5	12.3	89	2	US-07-927-391-6	Sequence 6, Appli	233	55.5	12.0	384	2	US-09-354-231B-18	Sequence 18, Appl
161	56.5	12.3	89	2	US-08-115-753-15	Sequence 15, Appl	234	55.5	12.0	384	2	US-09-128-602B-14	Sequence 14, Appl
162	56.5	12.3	158	2	US-09-107-532A-6092	Sequence 6092, Ap	235	55.5	12.0	384	2	US-09-128-602B-16	Sequence 16, Appl
163	56.5	12.3	168	2	US-09-898-659-16	Sequence 16, Appl	236	55.5	12.0	384	2	US-09-128-602B-18	Sequence 18, Appl
164	56.5	12.3	205	2	US-08-818-112-80	Sequence 80, Appl	237	55.5	12.0	384	2	US-09-995-297-14	Sequence 14, Appl
165	56.5	12.3	205	2	US-08-818-111-81	Sequence 81, Appl	238	55.5	12.0	384	2	US-09-995-297-16	Sequence 16, Appl
166	56.5	12.3	205	2	US-09-056-556-80	Sequence 80, Appl	239	55.5	12.0	384	2	US-09-995-297-18	Sequence 18, Appl
167	56.5	12.3	205	2	US-09-072-596-81	Sequence 81, Appl	240	55.5	12.0	384	2	US-09-771-904A-14	Sequence 14, Appl
168	56.5	12.3	205	2	US-09-072-596-80	Sequence 80, Appl	241	55.5	12.0	384	2	US-09-771-904A-16	Sequence 16, Appl
169	56.5	12.3	205	2	US-10-193-002-81	Sequence 81, Appl	242	55.5	12.0	384	2	US-09-771-904A-18	Sequence 18, Appl
170	56.5	12.3	205	2	US-10-084-843-80	Sequence 80, Appl	243	55.5	12.0	391	2	US-09-489-039A-9791	Sequence 9791, Ap
171	56.5	12.3	213	2	US-09-605-703B-2594	Sequence 2594, Ap	244	55.5	12.0	445	5	PCT-US94-05387-7	Sequence 7, Appli
172	56.5	12.3	233	2	US-08-818-112-76	Sequence 76, Appl	245	55.5	12.0	559	1	US-08-313-553-15	Sequence 15, Appl

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OM protein - protein search, using sw model

Run on: November 21, 2006, 19:44:48 ; Search time 53 Seconds  
(without alignments)  
146.985 Million cell updates/sec

Title: US-10-063-557-50

Perfect score: 461

Sequence: 1 MERVYIALLLAGLTALLEAN.....HSPVPEKAIPITPGSATTC 89

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : Issued Patents AA:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/5 COMB pep:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6 COMB pep:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7 COMB pep:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H COMB pep:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS COMB pep:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE COMB pep:\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pcp:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	461	100.0	89	2	US-09-289-349-11 Sequence 11, Appl
2	461	100.0	89	2	US-09-391-181-262 Sequence 262, Appl
3	461	100.0	89	2	US-09-444-444-262 Sequence 262, Appl
4	461	100.0	89	2	US-09-333-333-262 Sequence 262, Appl
5	461	100.0	89	2	US-09-992-598-262 Sequence 262, Appl
6	461	100.0	89	2	US-09-989-735-262 Sequence 262, Appl
7	461	100.0	89	3	US-09-989-726-262 Sequence 262, Appl
8	461	100.0	89	3	US-09-997-514-262 Sequence 262, Appl
9	461	100.0	89	3	US-09-989-728-262 Sequence 262, Appl
10	461	100.0	89	3	US-09-349-262 Sequence 262, Appl
11	461	100.0	89	3	US-09-997-653-262 Sequence 262, Appl
12	461	100.0	89	3	US-09-989-293A-262 Sequence 262, Appl
13	276.5	60.0	88	2	US-09-724-864-58 Sequence 58, Appl
14	256.5	55.6	87	1	US-08-725-531-5 Sequence 5, Appl
15	256.5	55.6	87	1	US-08-738-127-5 Sequence 5, Appl
16	256.5	55.6	87	1	US-09-213-392-5 Sequence 5, Appl
17	256.5	55.6	87	1	US-09-083-661-5 Sequence 5, Appl
18	214.5	46.5	87	1	US-08-289-247B-4 Sequence 4, Appl
19	214.5	46.5	87	1	US-08-725-531-4 Sequence 4, Appl
20	214.5	46.5	87	1	US-08-738-127-4 Sequence 4, Appl
21	214.5	46.5	87	1	US-09-213-392-4 Sequence 4, Appl
22	214.5	46.5	87	1	US-09-083-661-4 Sequence 4, Appl
23	214.5	46.5	124	2	US-09-949-016-8238 Sequence 8238, Ap
24	214.5	46.5	124	2	US-09-949-016-8239 Sequence 8239, Ap
25	191.5	41.5	178	2	US-09-949-016-9028 Sequence 9028, Ap
26	191.5	41.5	178	2	US-09-949-016-9029 Sequence 9029, Ap

27	131	28.4	106	2	US-09-621-976-5338 Sequence 5338, Ap
28	131	28.4	107	2	US-09-621-976-5332 Sequence 5332, Ap
29	129	28.0	92	1	US-08-738-127-1 Sequence 1, Appli
30	129	28.0	92	2	US-09-247-155-120 Sequence 120, App
31	129	28.0	92	2	US-09-148-545-238 Sequence 238, App
32	129	28.0	92	2	US-09-621-011-238 Sequence 238, App
33	129	28.0	92	2	US-09-903-190-120 Sequence 120, App
34	129	28.0	93	2	US-09-148-545-183 Sequence 183, App
35	129	28.0	93	2	US-09-621-011-183 Sequence 183, App
36	126.5	27.4	92	1	US-08-725-531-3 Sequence 3, Appli
37	126.5	27.4	92	1	US-08-738-127-3 Sequence 3, Appli
38	126.5	27.4	92	1	US-09-213-392-3 Sequence 3, Appli
39	126.5	27.4	92	1	US-09-083-661-3 Sequence 3, Appli
40	121	26.2	70	2	US-09-148-545-269 Sequence 269, App
41	121	26.2	70	2	US-09-621-011-269 Sequence 269, App
42	112.5	24.4	95	1	US-08-725-531-1 Sequence 1, Appli
43	112.5	24.4	95	1	US-09-213-392-1 Sequence 1, Appli
44	112.5	24.4	95	1	US-09-083-661-1 Sequence 1, Appli
45	112.5	24.4	96	2	US-09-149-476-473 Sequence 473, App
46	112.5	24.4	120	2	US-09-991-181-199 Sequence 199, App
47	112.5	24.4	120	2	US-09-990-444-199 Sequence 199, App
48	112.5	24.4	120	2	US-09-997-333-199 Sequence 199, App
49	112.5	24.4	120	2	US-09-992-598-199 Sequence 199, App
50	112.5	24.4	120	2	US-09-989-735-199 Sequence 199, App
51	112.5	24.4	120	3	US-09-989-726-199 Sequence 199, App
52	112.5	24.4	120	3	US-09-997-514-199 Sequence 199, App
53	112.5	24.4	120	3	US-09-989-728-199 Sequence 199, App
54	112.5	24.4	120	3	US-09-997-349-199 Sequence 199, App
55	112.5	24.4	120	3	US-09-997-653-199 Sequence 199, App
56	112.5	24.4	120	3	US-09-989-293A-199 Sequence 199, App
57	106	22.5	69	2	US-09-149-476-606 Sequence 606, App
58	103.5	22.5	95	2	US-09-621-976-5250 Sequence 5250, Ap
59	99.5	21.6	72	2	US-08-905-223-405 Sequence 405, App
60	94	20.4	179	2	US-09-205-258-424 Sequence 424, App
61	94	20.4	179	2	US-10-004-860-424 Sequence 424, App
62	89	19.3	80	2	US-09-621-976-6085 Sequence 6085, Ap
63	83	18.0	86	2	US-09-949-016-8419 Sequence 8419, Ap
64	83	18.0	86	2	US-09-949-016-8420 Sequence 8420, Ap
65	73.5	15.9	58	1	US-08-725-531-6 Sequence 6, Appli
66	73.5	15.9	58	1	US-08-738-127-6 Sequence 6, Appli
67	73.5	15.9	58	1	US-09-213-392-6 Sequence 6, Appli
68	73.5	15.9	58	1	US-09-083-661-6 Sequence 2, Appli
69	67.5	14.6	664	2	US-09-268-140-2 Sequence 9005, Ap
70	67.5	14.6	664	2	US-09-949-016-9005 Sequence 1112, Ap
71	66.5	14.4	376	2	US-09-198-452A-1112 Sequence 1038, Ap
72	66.5	14.4	388	2	US-09-438-185A-1038 Sequence 6195, Ap
73	66.5	14.4	523	2	US-09-949-016-6195 Sequence 1953, Ap
74	66.5	14.4	552	2	US-09-949-016-8164 Sequence 8164, Ap
75	65.5	14.2	546	2	US-10-094-749-1953 Sequence 1953, Ap
76	64.5	14.0	729	2	US-09-248-796A-17121 Sequence 17121, A
77	63	13.7	627	2	US-10-222-100-3 Sequence 3, Appli
78	62.5	13.6	339	2	US-09-690-454-66 Sequence 66, Appli
79	62.5	13.6	339	2	US-10-036-041-80 Sequence 80, Appl
80	62.5	13.6	339	3	US-10-062-831-66 Sequence 66, Appl
81	62.5	13.6	340	3	US-09-690-454-174 Sequence 174, App
82	62.5	13.6	340	3	US-10-062-831-174 Sequence 174, App
83	62.5	13.6	389	2	US-09-328-352-7324 Sequence 7324, Ap
84	62	13.4	78	2	US-09-749-637A-342 Sequence 342, App
85	62	13.4	360	2	US-09-489-039A-8000 Sequence 8000, Ap
86	62	13.4	601	2	US-09-336-643A-4 Sequence 4, Appli
87	62	13.4	638	2	US-10-154-419-61 Sequence 3725, Ap
88	61.5	13.3	103	2	US-09-107-532A-3725 Sequence 925, App
89	61.5	13.3	433	2	US-09-198-452A-925 Sequence 860, App
90	61.5	13.3	453	2	US-09-438-185A-860 Sequence 3, Appli
91	61.5	13.3	549	2	US-09-120-365-3 Sequence 3, Appli
92	61.5	13.3	549	2	US-09-515-035-3 Sequence 41830, A
93	61.5	13.3	606	2	US-09-270-767-41830 Sequence 7, Appli
94	61.5	13.3	990	2	US-10-363-937-7 Sequence 12762, A
95	61	13.2	457	2	US-09-489-038A-12762 Sequence 341, App
96	60.5	13.1	106	2	US-09-149-476-341 Sequence 13, Appl
97	60.5	13.1	288	2	US-09-386-642-13 Sequence 83, Appl
98	60.5	13.1	638	2	US-10-154-419-83 Sequence 28424, A
99	60.5	13.1	998	2	US-09-252-991A-28424 Sequence 28424, A

Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1498  
ID ADF74108 standard; protein; 178 AA.  
DE Human cell adhesion inhibitor protein disadherin.  
PN JP2003174885-A.  
PD 24-JUN-2003.  
PA (KOKU-) KOKURITSU GAN CENT SOCHO.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1499  
ID ADG12707 standard; protein; 178 AA.  
DE Novel human secreted and transmembrane protein PRO6241.  
PN US2003207392-A1.  
PD 06-NOV-2003.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1500  
ID ADH09367 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003207395-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;



PN US2003068694-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 20.4%; Score 94; DB 7; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0035;  
 RESULT 1480  
 ID ABO36977 standard; protein; 178 AA.  
 DE Human secreted/transmembrane protein (PRO) #271.  
 PN US2003068715-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 20.4%; Score 94; DB 7; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0035;  
 RESULT 1481  
 ID ABO37587 standard; protein; 178 AA.  
 DE Human secreted/transmembrane protein (PRO) #271.  
 PN US2003068726-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 20.4%; Score 94; DB 7; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0035;  
 RESULT 1482  
 ID ABM75377 standard; protein; 178 AA.  
 DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
 PN US2003104544-A1.  
 PD 05-JUN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 20.4%; Score 94; DB 7; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0035;  
 RESULT 1483  
 ID ABM33657 standard; protein; 178 AA.  
 DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
 PN US2003096357-A1.  
 PD 22-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 20.4%; Score 94; DB 7; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0035;  
 RESULT 1484  
 ID ABO46412 standard; protein; 178 AA.  
 DE Human PRO polypeptide #271.  
 PN US2003049760-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 20.4%; Score 94; DB 7; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0035;  
 RESULT 1485  
 ID ADA82977 standard; protein; 178 AA.  
 DE Human secreted/transmembrane protein (PRO) #271.  
 PN US2003049755-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 20.4%; Score 94; DB 7; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0035;  
 RESULT 1486  
 ID ADB91706 standard; protein; 178 AA.  
 DE Human secreted protein #SEQ ID 652.  
 PN WO2003004622-A2.  
 PD 16-JAN-2003.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 20.4%; Score 94; DB 7; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0035;  
 RESULT 1487  
 ID AEM32011 standard; protein; 178 AA.  
 DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
 PN US2003068680-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 20.4%; Score 94; DB 7; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0035;  
 RESULT 1488  
 ID ABM31401 standard; protein; 178 AA.  
 DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
 PN US2003068762-A1.  
 PD 10-APR-2003.

PA (GETH ) GENENTECH INC.  
 Query Match 20.4%; Score 94; DB 7; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0035;  
 RESULT 1489  
 ID ADB86285 standard; protein; 178 AA.  
 DE Human secreted/transmembrane protein (PRO) #271.  
 PN US2003054472-A1.  
 PD 20-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 20.4%; Score 94; DB 7; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0035;  
 RESULT 1490  
 ID ABM32316 standard; protein; 178 AA.  
 DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
 PN US2003068708-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 20.4%; Score 94; DB 7; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0035;  
 RESULT 1491  
 ID ABM32621 standard; protein; 178 AA.  
 DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
 PN US2003068713-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 20.4%; Score 94; DB 7; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0035;  
 RESULT 1492  
 ID ABM31706 standard; protein; 178 AA.  
 DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
 PN US2003068761-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 20.4%; Score 94; DB 7; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0035;  
 RESULT 1493  
 ID ABM31096 standard; protein; 178 AA.  
 DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
 PN US2003068771-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 20.4%; Score 94; DB 7; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0035;  
 RESULT 1494  
 ID ADD06015 standard; protein; 178 AA.  
 DE Human secreted/transmembrane protein (PRO) #271.  
 PN US2003087376-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 20.4%; Score 94; DB 7; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0035;  
 RESULT 1495  
 ID ADG03010 standard; protein; 178 AA.  
 DE Novel human secreted and transmembrane protein PRO6241.  
 PN US2003207397-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 20.4%; Score 94; DB 7; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0035;  
 RESULT 1496  
 ID ADG01717 standard; protein; 178 AA.  
 DE Novel human secreted and transmembrane protein PRO6241.  
 PN US2003207399-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 20.4%; Score 94; DB 7; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0035;  
 RESULT 1497  
 ID ADF95892 standard; protein; 178 AA.  
 DE Novel human secreted and transmembrane protein PRO6241.  
 PN US2003207398-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.

PN US2003068681-A1.  
PD 10-APR-2003.  
Query Match  
Best Local Similarity 20.4%; Score 94; DB 7; Length 178;  
PD 06-MAR-2003. Pred. No. 0.0035;  
RESULT 1461  
ID ABM74767 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003096351-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 20.4%; Score 94; DB 7; Length 178;  
PD 06-MAR-2003. Pred. No. 0.0035;  
RESULT 1462  
ID ABM33962 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003096358-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 20.4%; Score 94; DB 7; Length 178;  
PD 05-JUN-2003. Pred. No. 0.0035;  
RESULT 1463  
ID ABM20421 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003104556-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 20.4%; Score 94; DB 7; Length 178;  
PD 05-JUN-2003. Pred. No. 0.0035;  
RESULT 1464  
ID ABO48913 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003049756-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 20.4%; Score 94; DB 7; Length 178;  
PD 20-FEB-2003. Pred. No. 0.0035;  
RESULT 1465  
ID ABR72978 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003036122-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 20.4%; Score 94; DB 7; Length 178;  
PD 20-FEB-2003. Pred. No. 0.0035;  
RESULT 1466  
ID ABO15620 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003036121-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 20.4%; Score 94; DB 7; Length 178;  
PD 27-FEB-2003. Pred. No. 0.0035;  
RESULT 1467  
ID ABR85335 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003040065-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 20.4%; Score 94; DB 7; Length 178;  
PD 06-MAR-2003. Pred. No. 0.0035;  
RESULT 1468  
ID ABO15315 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003044919-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 20.4%; Score 94; DB 7; Length 178;  
PD 06-MAR-2003. Pred. No. 0.0035;  
RESULT 1469  
ID ABO17450 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003040077-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 20.4%; Score 94; DB 7; Length 178;  
PD 27-FEB-2003. Pred. No. 0.0035;  
RESULT 1470  
ID ABO41247 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.

ID ABM17739 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003044928-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 20.4%; Score 94; DB 7; Length 178;  
PD 06-MAR-2003. Pred. No. 0.0035;  
RESULT 1471  
ID ABR85640 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003049746-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 20.4%; Score 94; DB 7; Length 178;  
PD 13-MAR-2003. Pred. No. 0.0035;  
RESULT 1472  
ID ABR77206 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003054464-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 20.4%; Score 94; DB 7; Length 178;  
PD 20-MAR-2003. Pred. No. 0.0035;  
RESULT 1473  
ID ABO28385 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003064459-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 20.4%; Score 94; DB 7; Length 178;  
PD 03-APR-2003. Pred. No. 0.0035;  
RESULT 1474  
ID ABM23166 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068757-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 20.4%; Score 94; DB 7; Length 178;  
PD 10-APR-2003. Pred. No. 0.0035;  
RESULT 1475  
ID ABM30486 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068723-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 20.4%; Score 94; DB 7; Length 178;  
PD 10-APR-2003. Pred. No. 0.0035;  
RESULT 1476  
ID ABM21946 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068741-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 20.4%; Score 94; DB 7; Length 178;  
PD 10-APR-2003. Pred. No. 0.0035;  
RESULT 1477  
ID ABM21641 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068744-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 20.4%; Score 94; DB 7; Length 178;  
PD 10-APR-2003. Pred. No. 0.0035;  
RESULT 1478  
ID ABM15172 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068766-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 20.4%; Score 94; DB 7; Length 178;  
PD 10-APR-2003. Pred. No. 0.0035;  
RESULT 1479  
ID ABO41247 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.

PN US2003068686-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1442  
ID ABM09987 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003073178-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1443  
ID ABO39112 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003068774-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1444  
ID ABM34877 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003104538-A1.  
PD 05-JUN-2003.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1445  
ID ABO51353 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003049781-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1446  
ID ABO04179 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003036158-A1.  
PD 20-FEB-2003.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1447  
ID ABO10649 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003036151-A1.  
PD 20-FEB-2003.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1448  
ID ABR77892 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003040067-A1.  
PD 27-FEB-2003.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1449  
ID ABR79102 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003054456-A1.  
PD 20-MAR-2003.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1450  
ID ABO24196 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003054482-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1451  
ID ABO40332 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.

ID ABR93960 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003054457-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1452  
ID ABM02003 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003059883-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1453  
ID ABM78426 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003049764-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1454  
ID ABR90215 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003073177-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1455  
ID ABM27741 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003064442-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1456  
ID ABM13342 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003064450-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1457  
ID ABO32045 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003088731-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1458  
ID ABM14257 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068683-A1.  
PD 10-APR-2003.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1459  
ID ABM08462 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068754-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1460  
ID ABO40332 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.

DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003049739-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1433  
ID ABM01698 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003059882-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1434  
ID ABM02308 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003059884-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1435  
ID ABR87470 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068687-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1436  
ID ABM13037 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003073186-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1437  
ID ABM30791 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003064443-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1438  
ID ABM24691 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003064444-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1439  
ID ABO29605 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003068697-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1440  
ID ABO31435 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003068710-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1441  
ID ABM14562 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.

PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1404  
ID ABO40027 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003068689-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1405  
ID ABO50133 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003049776-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1406  
ID ABO51048 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003049780-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1407  
ID ABO05504 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003036126-A1.  
PD 20-FEB-2003.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1408  
ID ABR74808 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003044924-A1.  
PD 06-MAR-2003.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1409  
ID ABR77287 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003044927-A1.  
PD 06-MAR-2003.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1410  
ID ABM18044 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003040072-A1.  
PD 27-FEB-2003.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1411  
ID ABR96095 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003040073-A1.  
PD 27-FEB-2003.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1412  
ID ABO22028 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003054475-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1413  
ID ABO20198 standard; protein; 178 AA.

DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003032124-A1.  
PD 13-FEB-2003.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1414  
ID ABO24501 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003064467-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1415  
ID ABR86250 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003049759-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1416  
ID ABM10902 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003064455-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1417  
ID ABM76901 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003054465-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1418  
ID ABR89605 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003073170-A1.  
PD 17-APR-2003.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1419  
ID ABM12732 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003073176-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1420  
ID ABM06022 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068717-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1421  
ID ABO35147 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003068728-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1422  
ID ABM03223 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068764-A1.  
PD 10-APR-2003.

ID ABO30825 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003064466-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1386  
ID ABO31130 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003064468-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1387  
ID ABM27436 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068760-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1388  
ID ABM30181 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068769-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1389  
ID ABM5717 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003045700-A1.  
PD 06-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1390  
ID ABM15782 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068698-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1391  
ID ABM08767 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068759-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1392  
ID ABO42467 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003049748-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1393  
ID ABO38197 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003068765-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1394  
ID ABO46107 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068763-A1.

DE Human PRO polypeptide #271.  
PN US2003049754-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1395  
ID ABM66910 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068688-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1396  
ID ABE20654 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003082767-A1.  
PD 01-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1397  
ID ABM19811 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003104552-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1398  
ID ABO49523 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003049774-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1399  
ID ABO49828 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003049775-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1400  
ID ADA78906 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003073181-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1401  
ID AB388385 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068720-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1402  
ID ABM27131 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068739-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1403  
ID ABM03528 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068763-A1.

Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1366  
ID ABO47022 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003049762-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1367  
ID ABO47327 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003049765-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1368  
ID ADA83611 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003049752-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1369  
ID ABR71758 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003032133-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1370  
ID ABR72368 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003032136-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1371  
ID ABR98707 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003036129-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1372  
ID ABO07077 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003040053-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1373  
ID ABR85030 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003040057-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1374  
ID ABR73588 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003054467-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1375  
ID ABR76682 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003044932-A1.

PD 06-MAR-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1376  
ID ABR73283 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003027270-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1377  
ID ABM18349 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003054469-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1378  
ID ABO20808 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003032126-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1379  
ID ABO25551 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003054463-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1380  
ID ABO25856 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003054466-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1381  
ID ABR94265 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003059879-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1382  
ID ABR80172 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003049738-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1383  
ID ABM1512 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003064469-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1384  
ID ABO33119 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003064453-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1385



Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1347  
ID ABO51658 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003049766-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1348  
ID ABO51963 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003049767-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1349  
ID ABO50743 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003049779-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1350  
ID ABR79867 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003040059-A1.  
PD 27-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1351  
ID ABM17129 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003040078-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1352  
ID ABO18161 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003044918-A1.  
PD 06-MAR-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1353  
ID ABO21113 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003032132-A1.  
PD 13-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1354  
ID ABR97072 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003054462-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1355  
ID ABM12427 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003064445-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1356  
ID ABM16519 standard; protein; 178 AA.

DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003064449-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1357  
ID ABM24386 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003064441-A1.  
PD 03-APR-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1358  
ID ABM14867 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068696-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1359  
ID ABM04748 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068712-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1360  
ID ABM06937 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068730-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1361  
ID ABM09377 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003073174-A1.  
PD 17-APR-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1362  
ID ABO39417 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003068775-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1363  
ID ABM75682 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003104545-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1364  
ID ABM25606 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003104541-A1.  
PD 05-JUN-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1365  
ID ABM20116 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003104554-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.

RESULT 1328  
ID ABO22893 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003027265-A1.  
PD 06-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1329  
ID ABO23198 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003054461-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1330  
ID ABR92740 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003064446-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1331  
ID ABR81697 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003049744-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1332  
ID ABR78121 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003049783-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1333  
ID ABR89910 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003073171-A1.  
PD 17-APR-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1334  
ID ABR26826 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003032121-A1.  
PD 13-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1335  
ID AEM13952 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003064458-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1336  
ID ABO28690 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003064460-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1337  
ID ABO30520 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003064464-A1.

PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1338  
ID ABM07547 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068702-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1339  
ID ABM04138 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068734-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1340  
ID ABO37282 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003068719-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1341  
ID ABO41857 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003068729-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1342  
ID ABO35452 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003068738-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1343  
ID ABM25301 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003104540-A1.  
PD 05-JUN-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1344  
ID ABO47693 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003049742-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1345  
ID ABO47998 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003049747-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1346  
ID ABO48608 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003049750-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.

RESULT 1309  
ID ABM34267 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003096359-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1310  
ID ABM34572 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003100061-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1311  
ID ABM34572 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003100061-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1312  
ID ABO21418 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003032125-A1.  
PD 13-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1313  
ID ABO22333 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003054477-A1.  
PD 20-MAR-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1314  
ID ABR96767 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003054460-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1315  
ID ABR85945 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003049753-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1316  
ID ABR99927 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003049763-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1317  
ID ABM00783 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003073172-A1.  
PD 17-APR-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1318  
ID ABM00478 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003073172-A1.  
PD 17-APR-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1319  
ID ABO29910 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003068700-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1320  
ID ABM23776 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068736-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1321  
ID ABM29571 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068679-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1322  
ID ABO38502 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003068767-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1323  
ID ABO45802 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003073182-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1324  
ID ABM20726 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003104557-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1325  
ID ADA81813 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003092121-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1326  
ID ABO16840 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003027276-A1.  
PD 06-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1327  
ID ABO18466 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US200304920-A1.  
PD 06-MAR-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;

RESULT 1290  
ID ABM33047 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003073185-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1291  
ID ABM22861 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003087373-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1292  
ID ABM75072 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003096353-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1293  
ID ADA80086 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003073173-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1294  
ID ABR96462 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003054458-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1295  
ID ABM02613 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003059886-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1296  
ID ABR86555 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003049758-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1297  
ID ABR86860 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003049772-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1298  
ID AEM16824 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003064448-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1299  
ID ABM29876 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003064456-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1300  
ID ABO29300 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003068693-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1301  
ID ABM24081 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068735-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1302  
ID ABM23471 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068753-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1303  
ID ABM22251 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068742-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1304  
ID ABO37892 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003068756-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1305  
ID ABM28656 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003082715-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1306  
ID ABM28961 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003082716-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1307  
ID ABM66605 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068737-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1308  
ID ABM75987 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003104547-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;

DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
FN US2003068751-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1272  
ID ABO40942 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
FN US2003068684-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1273  
ID ABM35589 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
FN US2003073179-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1274  
ID ABM33352 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
FN US2003087374-A1.  
PD 08-MAY-2003.  
Query Match  
Best Local Similarity 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1275  
ID ABO52878 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
FN US2003049773-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1276  
ID ABO50438 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
FN US2003049777-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1277  
ID ABU99432 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
FN US2003040055-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1278  
ID ABO04484 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
FN US2003036164-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1279  
ID ABM18654 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
FN US2003054480-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1280  
ID ABR97682 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
FN US2003059885-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1281  
ID ABR80782 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
FN US2003049740-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1282  
ID ABM01393 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
FN US2003049770-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1283  
ID ABR88995 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
FN US2003073169-A1.  
PD 17-APR-2003.  
Query Match  
Best Local Similarity 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1284  
ID ABM13647 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
FN US2003064457-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1285  
ID ABM21031 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
FN US2003068711-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1286  
ID ABO42162 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
FN US2003049745-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1287  
ID ABO42772 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
FN US2003049751-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1288  
ID ABM10292 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
FN US2003067478-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1289  
ID ABO38807 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
FN US2003068773-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;

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Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1253
ID ABO09072 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1254
ID ABO36672 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1255
ID ABO35757 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1256
ID ABO39722 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1257
ID ABO10597 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003089407-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1258
ID ABO12122 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1259
ID ABO52268 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1260
ID ABO52573 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1261
ID ABO23891 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003032134-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1262
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ID ABR97377 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1263
ID ABR87165 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1264
ID ABM11207 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1265
ID ABM28351 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1266
ID ABO32350 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1267
ID ABM15477 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1268
ID ABO6632 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1269
ID ABM04443 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1270
ID ABM22556 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1271
ID ABM07852 standard; protein; 178 AA.
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PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1234  
ID ABM76596 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003082717-A1.  
PD 01-MAY-2003.  
Query Match  
Best Local Similarity 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1235  
ID ABM76292 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003104548-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1236  
ID ABM25911 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003104542-A1.  
PD 05-JUN-2003.  
Query Match  
Best Local Similarity 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1237  
ID ABM26216 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003104543-A1.  
PD 05-JUN-2003.  
Query Match  
Best Local Similarity 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1238  
ID ABO03569 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US20030316127-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1239  
ID ABO02654 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003040061-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1240  
ID ABR90825 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003036130-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1241  
ID ABR73893 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003054468-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1242  
ID ABO17145 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003054470-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1243  
ID ABR94570 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003044917-A1.

PD 06-MAR-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1244  
ID ABR76077 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003044929-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1245  
ID ABR71453 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003059880-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1246  
ID ABR93350 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003064465-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1247  
ID ABR93655 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003054478-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1248  
ID ABR88080 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068718-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1249  
ID ABO28080 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003064454-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1250  
ID ABO30215 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003064461-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1251  
ID ABO33424 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003068724-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1252  
ID ABM05112 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068727-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;



DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003064440-A1.  
PD 03-APR-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1216  
ID ABM06327 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068704-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1217  
ID ABM03833 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068722-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1218  
ID ABM35284 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003073183-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1219  
ID ABM6521 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003104549-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1220  
ID ABO48303 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003049749-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1221  
ID ABR93045 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003084462-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1222  
ID ABO24806 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003065159-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1223  
ID ABM11817 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003064447-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1224  
ID ABM02918 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003073184-A1.

PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1225  
ID ABM16214 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003064463-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1226  
ID ABO27775 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003064451-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1227  
ID ABM29266 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068721-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1228  
ID ABM07242 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068699-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1229  
ID ABM21336 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068707-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1230  
ID ABM09682 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003073175-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1231  
ID ABO41552 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003068695-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1232  
ID ABO36367 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003068703-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1233  
ID ABO43896 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003068732-A1.  
PD 10-APR-2003.

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PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1206
ID ABO03264 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US20030306131-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1207
ID ABR90520 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1208
ID ABR95180 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1209
ID ABR95180 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US200304930-A1.
PD 06-MAR-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1210
ID ABR95485 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1211
ID ABO21723 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1212
ID ABR97987 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1213
ID ABR87775 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1214
ID ABM77816 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1215
ID ABM28046 standard; protein; 178 AA.
PD 05-JUN-2003.

PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1197
ID ABM77511 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1198
ID ABO28995 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1199
ID ABO31740 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1200
ID ABM08157 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1201
ID ABO40637 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1202
ID ABO36062 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1203
ID ABO44201 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1204
ID ADA78294 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1205
ID ABM24996 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003104539-A1.
PD 05-JUN-2003.
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Query Match      20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1177
ID ABU91624 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match      20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1178
ID ABU84838 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match      20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1179
ID ABR69928 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match      20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1180
ID ABU80305 standard; protein; 178 AA.
DE Human PRO protein #271.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match      20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1181
ID ABU93574 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match      20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1182
ID ABO10127 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match      20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1183
ID ABO09212 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match      20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1184
ID ABU10780 standard; protein; 178 AA.
DE Human secreted/transmembrane protein #271.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match      20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1185
ID ABU95789 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match      20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1186
ID ABU96998 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match      20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1187
ID ABR70843 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1188
ID ABO05194 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1189
ID ABO08602 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match      20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1190
ID ABO05809 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match      20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1191
ID ABR74198 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match      20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1192
ID ABR95790 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1193
ID ABR81087 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1194
ID ABR81392 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1195
ID ABM01088 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1196
ID ABR88690 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068743-A1.
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ID ABR66712 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003027281-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1157  
ID ABR91130 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003040058-A1.  
PD 27-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1158  
ID ABU94557 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003017540-A1.  
PD 23-JAN-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1159  
ID ABU79439 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003032106-A1.  
PD 13-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1160  
ID ABU86768 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003032129-A1.  
PD 13-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1161  
ID ABU87073 standard; protein; 178 AA.  
DE Novel human secreted and transmembrane protein PRO6241.  
PN US2003032131-A1.  
PD 13-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1162  
ID ABU94862 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003032103-A1.  
PD 13-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1163  
ID ABO04789 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003032107-A1.  
PD 13-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1164  
ID ABR70538 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003032139-A1.  
PD 13-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1165  
ID ABU98703 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003022301-A1.  
PD 30-JAN-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1166  
ID ABR66102 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.

PN US2003036165-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1167  
ID ABR64819 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003027262-A1.  
PD 06-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1168  
ID ABU79744 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003032110-A1.  
PD 13-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1169  
ID ABU93135 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003036142-A1.  
PD 20-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1170  
ID ABU96094 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003036145-A1.  
PD 20-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1171  
ID ABU91314 standard; protein; 178 AA.  
DE Novel human secreted and transmembrane protein PRO6241.  
PN US2003036154-A1.  
PD 20-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1172  
ID ABU90407 standard; protein; 178 AA.  
DE Novel human secreted and transmembrane protein PRO6241.  
PN US2003036153-A1.  
PD 20-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1173  
ID ABO09822 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003044931-A1.  
PD 06-MAR-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1174  
ID ABO11094 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003036150-A1.  
PD 20-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1175  
ID ABR71148 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003040069-A1.  
PD 27-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1176  
ID ABU87756 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003022293-A1.  
PD 30-JAN-2003.

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PN US2003022297-A1.
PD 30-JAN-2003.
Query Match      20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1136
ID ABU83113 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match      20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1137
ID ABU95169 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match      20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1138
ID ABU90717 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match      20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1139
ID ABU84228 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match      20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1140
ID ABU93879 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003032119-A1.
PD 13-FEB-2003.
Query Match      20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1141
ID ABR65124 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match      20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1142
ID ABR68956 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match      20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1143
ID ABO06772 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match      20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1144
ID ABR99317 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match      20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1145
ID ABU57201 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match      20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1146
ID ABU86153 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match      20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1147
ID ABU82440 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match      20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1148
ID ABU87451 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match      20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1149
ID ABU83923 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match      20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1150
ID ABO08297 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match      20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1151
ID ABU82008 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match      20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1152
ID ABU66172 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match      20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1153
ID ABR60001 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match      20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1154
ID ABU94189 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match      20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1155
ID ABO00062 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match      20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1156
```

ID ABU65839 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein, SEQ ID 542.  
PN US2003036156-A1.  
PD 20-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1116  
ID AB007687 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003032117-A1.  
PD 13-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1117  
ID AB003874 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003036128-A1.  
PD 20-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1118  
ID ABR67322 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003027266-A1.  
PD 06-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1119  
ID ABR67322 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003054483-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1120  
ID ABU56206 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein, PRO6241.  
PN US2003022298-A1.  
PD 30-JAN-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1121  
ID ABU65534 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003032102-A1.  
PD 13-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1122  
ID ABU95479 standard; protein; 178 AA.  
DE Novel human secreted and transmembrane protein PRO6241.  
PN US2003036117-A1.  
PD 20-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1123  
ID ABU71382 standard; protein; 178 AA.  
DE Human PRO6241 protein.  
PN US2003036143-A1.  
PD 20-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1124  
ID AB007992 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003032130-A1.  
PD 13-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1125  
ID ABR70233 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.

PN US2003032138-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1126  
ID ABR69566 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003036132-A1.  
PD 20-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1127  
ID AB001707 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003008353-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1128  
ID ABU81509 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003017542-A1.  
PD 23-JAN-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1129  
ID ABR60306 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003032137-A1.  
PD 13-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1130  
ID ABR68041 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003027269-A1.  
PD 06-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1131  
ID ABR65429 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003027268-A1.  
PD 06-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1132  
ID ABR68651 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003027274-A1.  
PD 06-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1133  
ID ABR72063 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003032135-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1134  
ID ABU85543 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003022295-A1.  
PD 30-JAN-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1135  
ID ABU89233 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.

Query Match 20.4%; Score 94; DB 6; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0035;  
 RESULT 1095  
 ID ABR99012 standard; protein; 178 AA.  
 DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
 PN US2003040064-A1.  
 PD 27-FEB-2003.  
 Query Match 20.4%; Score 94; DB 6; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0035;  
 RESULT 1096  
 ID ABO16535 standard; protein; 178 AA.  
 DE Human secreted/transmembrane protein (PRO) #271.  
 PN US2003027267-A1.  
 PD 06-FEB-2003.  
 Query Match 20.4%; Score 94; DB 6; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0035;  
 RESULT 1097  
 ID ABR92435 standard; protein; 178 AA.  
 DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
 PN US2003036160-A1.  
 PD 20-FEB-2003.  
 Query Match 20.4%; Score 94; DB 6; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0035;  
 RESULT 1098  
 ID ABO19076 standard; protein; 178 AA.  
 DE Human secreted/transmembrane protein (PRO) #271.  
 PN US2003044925-A1.  
 PD 06-MAR-2003.  
 Query Match 20.4%; Score 94; DB 6; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0035;  
 RESULT 1099  
 ID ABR78497 standard; protein; 178 AA.  
 DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
 PN US2003054474-A1.  
 PD 20-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 20.4%; Score 94; DB 6; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0035;  
 RESULT 1100  
 ID ABUS5233 standard; protein; 178 AA.  
 DE Novel human secreted and transmembrane protein PRO6241.  
 PN US2003032114-A1.  
 PD 13-FEB-2003.  
 Query Match 20.4%; Score 94; DB 6; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0035;  
 RESULT 1101  
 ID ABO00372 standard; protein; 178 AA.  
 DE Novel human secreted and transmembrane protein PRO6241.  
 PN US2003032101-A1.  
 PD 13-FEB-2003.  
 Query Match 20.4%; Score 94; DB 6; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0035;  
 RESULT 1102  
 ID ABO11704 standard; protein; 178 AA.  
 DE Human secreted/transmembrane protein (PRO) #271.  
 PN US2003036124-A1.  
 PD 20-FEB-2003.  
 Query Match 20.4%; Score 94; DB 6; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0035;  
 RESULT 1103  
 ID ABO02349 standard; protein; 178 AA.  
 DE Human secreted/transmembrane protein (PRO) #271.  
 PN US2003040054-A1.  
 PD 27-FEB-2003.  
 Query Match 20.4%; Score 94; DB 6; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0035;  
 RESULT 1104  
 ID ADA41202 standard; protein; 178 AA.  
 DE Human secreted protein.  
 PN WO2002102993-A2.  
 PD 27-DSC-2002.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 20.4%; Score 94; DB 6; Length 178;

Best Local Similarity 43.9%; Pred. No. 0.0035;  
 RESULT 1105  
 ID ABUS8923 standard; protein; 178 AA.  
 DE Novel human secreted and transmembrane protein PRO6241.  
 PN US2003036133-A1.  
 PD 20-FEB-2003.  
 Query Match 20.4%; Score 94; DB 6; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0035;  
 RESULT 1106  
 ID ABUS3618 standard; protein; 178 AA.  
 DE Human secreted/transmembrane protein (PRO) #271.  
 PN US2003036134-A1.  
 PD 20-FEB-2003.  
 Query Match 20.4%; Score 94; DB 6; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0035;  
 RESULT 1107  
 ID ABO06419 standard; protein; 178 AA.  
 DE Novel human secreted and transmembrane protein PRO6241.  
 PN US2003022294-A1.  
 PD 30-JAN-2003.  
 Query Match 20.4%; Score 94; DB 6; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0035;  
 RESULT 1108  
 ID ABR59455 standard; protein; 178 AA.  
 DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
 PN US2003027275-A1.  
 PD 06-FEB-2003.  
 Query Match 20.4%; Score 94; DB 6; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0035;  
 RESULT 1109  
 ID ABO09517 standard; protein; 178 AA.  
 DE Human secreted/transmembrane protein (PRO) #271.  
 PN US2003027324-A1.  
 PD 06-FEB-2003.  
 Query Match 20.4%; Score 94; DB 6; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0035;  
 RESULT 1110  
 ID ABO19381 standard; protein; 178 AA.  
 DE Novel human secreted and transmembrane protein PRO6241.  
 PN US2003036118-A1.  
 PD 20-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 20.4%; Score 94; DB 6; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0035;  
 RESULT 1111  
 ID ABO11399 standard; protein; 178 AA.  
 DE Human secreted/transmembrane protein (PRO) #271.  
 PN US2003036123-A1.  
 PD 20-FEB-2003.  
 Query Match 20.4%; Score 94; DB 6; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0035;  
 RESULT 1112  
 ID ABR67017 standard; protein; 178 AA.  
 DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
 PN US2003036148-A1.  
 PD 20-FEB-2003.  
 Query Match 20.4%; Score 94; DB 6; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0035;  
 RESULT 1113  
 ID ABO16230 standard; protein; 178 AA.  
 DE Human secreted/transmembrane protein (PRO) #271.  
 PN US2003040060-A1.  
 PD 27-FEB-2003.  
 Query Match 20.4%; Score 94; DB 6; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0035;  
 RESULT 1114  
 ID ABO13936 standard; protein; 178 AA.  
 DE Human secreted/transmembrane protein (PRO) #271.  
 PN US2003044916-A1.  
 PD 06-MAR-2003.  
 Query Match 20.4%; Score 94; DB 6; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0035;  
 RESULT 1115



PN US2003027278-A1.  
PD 06-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1075  
ID ABR65797 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003036159-A1.  
PD 20-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1076  
ID ABU9737 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003040070-A1.  
PD 27-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1077  
ID ABU82976 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003032113-A1.  
PD 13-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1078  
ID ABU90097 standard; protein; 178 AA.  
DE Novel human secreted and transmembrane protein PRO6241.  
PN US2003036147-A1.  
PD 20-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1079  
ID ABR68346 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003027264-A1.  
PD 06-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1080  
ID ABU96399 standard; protein; 178 AA.  
DE Novel human secreted and transmembrane protein PRO6241.  
PN US2003036144-A1.  
PD 20-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1081  
ID ABU92830 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003036149-A1.  
PD 20-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1082  
ID AB008907 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003044923-A1.  
PD 06-MAR-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1083  
ID AB002959 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003040062-A1.  
PD 27-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1084  
ID ABR75113 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003040056-A1.  
PD 27-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;

Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1085  
ID ABR94875 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003044926-A1.  
PD 06-MAR-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1086  
ID ABU85848 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003036140-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1087  
ID ABU99008 standard; protein; 178 AA.  
DE Novel human secreted and transmembrane protein PRO6241.  
PN US2003013153-A1.  
PD 16-JAN-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1088  
ID ABU98223 standard; protein; 178 AA.  
DE Novel human secreted and transmembrane protein PRO6241.  
PN US2003017544-A1.  
PD 23-JAN-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1089  
ID ABU91929 standard; protein; 178 AA.  
DE Novel human secreted and transmembrane protein PRO6241.  
PN US2003027277-A1.  
PD 06-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1090  
ID ABU89622 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003036141-A1.  
PD 20-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1091  
ID ABU86463 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003036146-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1092  
ID ABU67676 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003036162-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1093  
ID ABU80704 standard; protein; 178 AA.  
DE Human PRO protein #271.  
PN US2003036137-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1094  
ID ABR99622 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003040063-A1.  
PD 27-FEB-2003.

Best Local Similarity 40.0%; Pred. No. 3.1e-05;  
RESULT 1056  
ID ADH74323 standard; protein; 69 AA.  
DE Human secreted protein #287.  
PN US2003225248-A1.  
PD 04-DEC-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 23.0%; Score 106; DB 8; Length 69;  
Best Local Similarity 40.0%; Pred. No. 3.1e-05;  
RESULT 1057  
ID ABG26346 standard; protein; 110 AA.  
DE Novel human diagnostic protein #26337.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 22.9%; Score 105.5; DB 4; Length 110;  
Best Local Similarity 33.8%; Pred. No. 6.5e-05;  
RESULT 1058  
ID AAY13121 standard; protein; 72 AA.  
DE Human secreted protein encoded by 5' EST SEQ ID NO: 135.  
PN WO9906552-A2.  
PD 11-FEB-1999.  
PA (GEST) GENSET.  
Query Match 21.6%; Score 99.5; DB 2; Length 72;  
Best Local Similarity 36.4%; Pred. No. 0.00022;  
RESULT 1059  
ID ABP03457 standard; protein; 63 AA.  
DE Human ORFX protein sequence SEQ ID NO: 6896.  
PN WO200192523-A2.  
PD 06-DEC-2001.  
PA (CURA-) CURAGEN CORP.  
Query Match 20.8%; Score 96; DB 5; Length 63;  
Best Local Similarity 32.8%; Pred. No. 0.00051;  
RESULT 1060  
ID ABG75825 standard; protein; 80 AA.  
DE Transporters and ion channels protein 7, TRICH-7.  
PN WO2003016493-A2.  
PD 27-FEB-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 20.6%; Score 95; DB 6; Length 80;  
Best Local Similarity 31.3%; Pred. No. 0.00092;  
RESULT 1061  
ID ABM85184 standard; protein; 148 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO: 5433.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 20.6%; Score 95; DB 8; Length 148;  
Best Local Similarity 36.8%; Pred. No. 0.002;  
RESULT 1062  
ID ABR82718 standard; protein; 115 AA.  
DE Human IWU-1 protein.  
PN WO2003064603-A2.  
PD 07-AUG-2003.  
PA (UTRP) UNIV ROCHESTER.  
Query Match 20.4%; Score 94; DB 7; Length 115;  
Best Local Similarity 43.9%; Pred. No. 0.002;  
RESULT 1063  
ID ABM85185 standard; protein; 147 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO: 5434.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 20.4%; Score 94; DB 8; Length 147;  
Best Local Similarity 43.9%; Pred. No. 0.0027;  
RESULT 1064  
ID AAY13945 standard; protein; 178 AA.  
DE Human transmembrane protein, HP10479.  
PN WO9918203-A2.  
PD 15-APR-1999.  
PA (SAGA) SAGAMI CHEM RES CENT.  
PA (PROT-) PROTEGENE INC.  
Query Match 20.4%; Score 94; DB 2; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1065  
ID AAY41674 standard; protein; 178 AA.  
DE Human channel-related molecule HCRM-2.  
PN WO9943807-A2.  
PD 02-SEP-1999.  
PA (INCY-) INCYTE PHARM INC.  
Query Match 20.4%; Score 94; DB 2; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1066  
ID AAU29294 standard; protein; 178 AA.  
DE Human PRO polypeptide sequence #271.  
PN WO200168848-A2.  
PD 20-SEP-2001.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 4; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1067  
ID AAM38819 standard; protein; 178 AA.  
DE Human polypeptide SEQ ID NO 1964.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 20.4%; Score 94; DB 4; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1068  
ID ABB90357 standard; protein; 178 AA.  
DE Human polypeptide SEQ ID NO 2733.  
PN WO200190304-A2.  
PD 29-NOV-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 20.4%; Score 94; DB 5; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1069  
ID AAO17172 standard; protein; 178 AA.  
DE Human secreted protein SEQ ID NO: 71.  
PN WO200228877-A1.  
PD 11-APR-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 20.4%; Score 94; DB 5; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1070  
ID ABG64783 standard; protein; 178 AA.  
DE Human albumin fusion protein #1458.  
PN WO200177137-A1.  
PD 18-OCT-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 20.4%; Score 94; DB 5; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1071  
ID ABUS8670 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003027272-A1.  
PD 06-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1072  
ID ABUS8670 standard; protein; 178 AA.  
DE Novel human secreted and transmembrane protein PRO6241.  
PN US2003032127-A1.  
PD 13-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1073  
ID ABUS8670 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003032112-A1.  
PD 13-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0035;  
RESULT 1074  
ID ABR66407 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO: 542.

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Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1046
ID AD03354 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2004214269-A1.
PD 28-OCT-2004.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1047
ID AD203405 standard; protein; 120 AA.
DE Human secreted/transmembrane PRO1056 protein.
PN US2005074837-A1.
PD 07-APR-2005.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 9; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1048
ID AEA38462 standard; protein; 120 AA.
DE Human secreted/transmembrane protein, #118.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 9; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1049
ID AEB14151 standard; protein; 120 AA.
DE Cancer cell diagnosis method-related human protein - SEQ ID 434.
PN US2005153396-A1.
PD 14-JUL-2005.
PA (BAKE/) BAKER K P.
PA (BERE/) BERESINI M.
PA (DEFO/) DEFOURGE L.
PA (DESN/) DESNOYERS L.
PA (FILV/) FILVARSOFF E.
PA (GAOW/) GAO W.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOSKI P J.
PA (GURN/) GURNEY A L.
PA (SHER/) SHERWOOD S.
PA (SMIT/) SMITH V.
PA (STEW/) STEWART T A.
PA (TUNA/) TUNAS D.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
PA (ZHAN/) ZHANG Z.
Query Match 24.4%; Score 112.5; DB 9; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1050
ID AED86349 standard; protein; 120 AA.
DE Human PRO amino acid sequence, seq id 434.
PN US2005245730-A1.
PD 03-NOV-2005.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 9; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1051
ID ABB80585 standard; protein; 95 AA.
DE Human sbg1015258PLM protein.
PN WO200222802-A1.
PD 21-MAR-2002.
PA (SMIK ) SMITHKLINE BEECHAM CORP.
PA (SMIK ) SMITHKLINE BEECHAM PLC.
PA (GLAX ) GLAXO GROUP LTD.
Query Match 24.3%; Score 112; DB 5; Length 95;
Best Local Similarity 35.9%; Pred. No. 8.1e-06;
RESULT 1052
ID AAW75005 standard; protein; 69 AA.
DE Human secreted protein encoded by gene 154 clone HB6FL83.
PN WO9839448-A2.
PD 11-SEP-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 23.0%; Score 106; DB 7; Length 69;
Best Local Similarity 40.0%; Pred. No. 3.1e-05;
RESULT 1053
ID ABG95466 standard; protein; 69 AA.
DE Human novel secreted protein #287.
PN US6420526-B1.
PD 16-JUL-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 23.0%; Score 106; DB 5; Length 69;
Best Local Similarity 40.0%; Pred. No. 3.1e-05;
RESULT 1054
ID ABO34660 standard; protein; 69 AA.
DE Region of human secreted protein encoded by cDNA sequence #287.
PN US2003049618-A1.
PD 13-MAR-2003.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (CART/) CARTER K C.
PA (BEDN/) BEDNARIK D P.
PA (ENDR/) ENDRESS G A.
PA (YUGG/) YU G.
PA (NIJJ/) NI J.
PA (FENG/) FENG P.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (DUAN/) DUAN D R.
PA (HUJJ/) HU J.
PA (FLOR/) FLORENCE K A.
PA (OLSE/) OLSEN H S.
PA (FISC/) FISCHER C L.
PA (EBNE/) EBNER R.
PA (BREW/) BREWER L A.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (LAFL/) LAFLEUR D W.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
Query Match 23.0%; Score 106; DB 6; Length 69;
Best Local Similarity 40.0%; Pred. No. 3.1e-05;
RESULT 1055
ID AD123321 standard; protein; 69 AA.
DE Novel human secreted protein seq id 606.
PN US2003175858-A1.
PD 18-SEP-2003.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (CART/) CARTER K C.
PA (BEDN/) BEDNARIK D P.
PA (ENDR/) ENDRESS G A.
PA (YUGG/) YU G.
PA (NIJJ/) NI J.
PA (FENG/) FENG P.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (DUAN/) DUAN D R.
PA (HUJJ/) HU J.
PA (FLOR/) FLORENCE K A.
PA (OLSE/) OLSEN H S.
PA (FISC/) FISCHER C L.
PA (EBNE/) EBNER R.
PA (BREW/) BREWER L A.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (LAFL/) LAFLEUR D W.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
Query Match 23.0%; Score 106; DB 7; Length 69;
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PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 1028  
ID ADH28614 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003022331-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 1029  
ID ADG54759 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US20030207367-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 1030  
ID ADG59799 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US20030207369-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 1031  
ID ADI18223 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US20030207361-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 1032  
ID ADG09966 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2004009548-A1.  
PD 15-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 1033  
ID ADI15437 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US20030207382-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 1034  
ID ADG09314 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2004009547-A1.  
PD 15-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 1035  
ID ADI14769 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US20030207383-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 1036  
ID ADI18364 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US20030207349-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.

Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 1037  
ID ADJ63645 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2004039164-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 1038  
ID ADJ77540 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2004038336-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 1039  
ID ADJ65662 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2004038335-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 1040  
ID ADM27798 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2004048333-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 1041  
ID ADM42522 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2004058424-A1.  
PD 25-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 1042  
ID ADM28384 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2004077064-A1.  
PD 22-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 1043  
ID ADI95866 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003077659-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 1044  
ID ADI96418 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US20030207354-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 1045  
ID ADS32370 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US20040203125-A1.  
PD 14-OCT-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;

ID ADG56967 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003207364-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 1010  
ID ADG55863 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003207365-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 1011  
ID ADG58623 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003207368-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 1012  
ID ADG70989 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003207420-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 1013  
ID ADG58071 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003207363-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 1014  
ID ADG53655 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003207415-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 1015  
ID ADG71541 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003207421-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 1016  
ID ADG81728 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003207805-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 1017  
ID ADH19445 standard; protein; 120 AA.  
DE Human secreted/transmembrane protein PRO1056.  
PN US2003228656-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 1018  
ID ADH30690 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.

PN US2003077723-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 1019  
ID ADH12057 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003207419-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 1020  
ID ADG52479 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003207414-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 1021  
ID ADG54207 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003207416-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 1022  
ID ADG81176 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003194793-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 1023  
ID ADG56415 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003207366-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 1024  
ID ADH12681 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003207378-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 1025  
ID ADH20938 standard; protein; 120 AA.  
DE Human secreted/transmembrane protein PRO1056.  
PN US2003224358-A1.  
PD 04-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 1026  
ID ADG61527 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003207429-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 1027  
ID ADH19978 standard; protein; 120 AA.  
DE Human secreted/transmembrane protein PRO1056.  
PN US2003219856-A1.  
PD 27-NOV-2003.

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Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 991
ID ADG16820 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 992
ID ADG05279 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 993
ID ADG19546 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 994
ID ADG13383 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 995
ID ADG08440 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 996
ID ADG15610 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 997
ID ADF97008 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 998
ID ADG06193 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 999
ID ADG23777 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1000
ID ADG04066 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1001
ID ADG24967 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1002
ID ADG07264 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1003
ID ADG07816 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1004
ID ADG55311 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1005
ID ADG60975 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1006
ID ADG62079 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1007
ID ADG82280 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1008
ID ADG57519 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1009
ID ADG57519 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
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PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 973
ID ADE94765 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 974
ID ADE91176 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 975
ID ADF35325 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003194760-A1.
PD 16-OCT-2003.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 976
ID ADE95317 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 977
ID ADE93427 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 978
ID ADFJ5008 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 979
ID ADE92323 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 980
ID ADE90624 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 981
ID ADE91771 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 982
ID ADG11575 standard; protein; 120 AA.
DE Human PRO polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 983
ID ADG02350 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 984
ID ADG22136 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 985
ID ADG20206 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 986
ID ADF98112 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 987
ID ADG24329 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 988
ID ADF98683 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 989
ID ADG03514 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 990
ID ADF99235 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
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ID ADH99872 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003049682-A1.  
PD 13-MAR-2003.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 955  
ID ADH81445 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003207377-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 956  
ID ADM82614 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003087355-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 957  
ID ADN16013 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003087353-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 958  
ID ADN16642 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003087385-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 959  
ID ADN15461 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003087356-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 960  
ID ADN14909 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003087357-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 961  
ID ADC81171 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003092115-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 962  
ID ADD76619 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003100087-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 963  
ID ADD87983 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.

PN US2003092113-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 964  
ID ADD86387 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003203440-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 965  
ID ADE75835 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003211571-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 966  
ID ADE23411 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003092108-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 967  
ID ADE23963 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003092110-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 968  
ID ADE24606 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003092111-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 969  
ID ADD87431 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003203439-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 970  
ID ADE89297 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003199062-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 971  
ID ADE18436 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003194794-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 972  
ID ADE88745 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003199054-A1.

Query Match	24.4%;	Score 112.5;	DB 7;	Length 120;
Best Local Similarity	36.0%;	Pred. No. 9.4e-06;		
RESULT 936				
ID ADH80635 standard; protein;	120 AA.			
DE Human PRO polypeptide #217.				
PN US2003207418-A1.				
PD 06-NOV-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	24.4%;	Score 112.5;	DB 7;	Length 120;
Best Local Similarity	36.0%;	Pred. No. 9.4e-06;		
RESULT 937				
ID ADH89663 standard; protein;	120 AA.			
DE Human PRO polypeptide #217.				
PN US2003199028-A1.				
PD 23-OCT-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	24.4%;	Score 112.5;	DB 7;	Length 120;
Best Local Similarity	36.0%;	Pred. No. 9.4e-06;		
RESULT 938				
ID ADE40947 standard; protein;	120 AA.			
DE Human PRO polypeptide #217.				
PN US2003199031-A1.				
PD 23-OCT-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	24.4%;	Score 112.5;	DB 7;	Length 120;
Best Local Similarity	36.0%;	Pred. No. 9.4e-06;		
RESULT 939				
ID ADE04746 standard; protein;	120 AA.			
DE Human PRO polypeptide #217.				
PN US2003199034-A1.				
PD 23-OCT-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	24.4%;	Score 112.5;	DB 7;	Length 120;
Best Local Similarity	36.0%;	Pred. No. 9.4e-06;		
RESULT 940				
ID ABE92875 standard; protein;	120 AA.			
DE Human PRO polypeptide #217.				
PN US2003194777-A1.				
PD 16-OCT-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	24.4%;	Score 112.5;	DB 7;	Length 120;
Best Local Similarity	36.0%;	Pred. No. 9.4e-06;		
RESULT 941				
ID ADF67126 standard; protein;	120 AA.			
DE Human PRO1056 amino acid sequence SEQ ID NO:199.				
PN US2002198148-A1.				
PD 26-DEC-2002.				
PA (GETH ) GENENTECH INC.				
Query Match	24.4%;	Score 112.5;	DB 7;	Length 120;
Best Local Similarity	36.0%;	Pred. No. 9.4e-06;		
RESULT 942				
ID ADG21584 standard; protein;	120 AA.			
DE Novel human secreted and transmembrane protein PRO1056.				
PN US2003207355-A1.				
PD 06-NOV-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	24.4%;	Score 112.5;	DB 7;	Length 120;
Best Local Similarity	36.0%;	Pred. No. 9.4e-06;		
RESULT 943				
ID ADG23225 standard; protein;	120 AA.			
DE Novel human secreted and transmembrane protein PRO1056.				
PN US2003207384-A1.				
PD 06-NOV-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	24.4%;	Score 112.5;	DB 7;	Length 120;
Best Local Similarity	36.0%;	Pred. No. 9.4e-06;		
RESULT 944				
ID ADF97560 standard; protein;	120 AA.			
DE Human PRO polypeptide #217.				
PN US2003207370-A1.				
PD 06-NOV-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	24.4%;	Score 112.5;	DB 7;	Length 120;
Best Local Similarity	36.0%;	Pred. No. 9.4e-06;		
RESULT 945				
ID ADF97560 standard; protein;	120 AA.			
DE Human PRO polypeptide #217.				
PN US2003207370-A1.				
PD 06-NOV-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	24.4%;	Score 112.5;	DB 7;	Length 120;

Best Local Similarity	36.0%;	Pred. No. 9.4e-06;
RESULT 945		
ID	ADG80624 standard; protein; 120 AA.	
DE	Human PRO polypeptide #217.	
PN	US2003207373-A1.	
PD	06-NOV-2003.	
PA	(GETH ) GENENTECH INC.	
Query Match	24.4%;	Score 112.5; DB 7; Length 120;
Best Local Similarity	36.0%;	Pred. No. 9.4e-06;
RESULT 946		
ID	ADG80072 standard; protein; 120 AA.	
DE	Human PRO polypeptide #217.	
PN	US2003207372-A1.	
PD	06-NOV-2003.	
PA	(GETH ) GENENTECH INC.	
Query Match	24.4%;	Score 112.5; DB 7; Length 120;
Best Local Similarity	36.0%;	Pred. No. 9.4e-06;
RESULT 947		
ID	ADH55364 standard; protein; 120 AA.	
DE	Novel human secreted and transmembrane protein PRO1056.	
PN	US2003207381-A1.	
PD	06-NOV-2003.	
PA	(GETH ) GENENTECH INC.	
Query Match	24.4%;	Score 112.5; DB 7; Length 120;
Best Local Similarity	36.0%;	Pred. No. 9.4e-06;
RESULT 948		
ID	ADH55916 standard; protein; 120 AA.	
DE	Novel human secreted and transmembrane protein PRO1056.	
PN	US2003207379-A1.	
PD	06-NOV-2003.	
PA	(GETH ) GENENTECH INC.	
Query Match	24.4%;	Score 112.5; DB 7; Length 120;
Best Local Similarity	36.0%;	Pred. No. 9.4e-06;
RESULT 949		
ID	ADI35380 standard; protein; 120 AA.	
DE	Human PRO polypeptide #50.	
PN	US2003050457-A1.	
PD	13-MAR-2003.	
PA	(GETH ) GENENTECH INC.	
Query Match	24.4%;	Score 112.5; DB 7; Length 120;
Best Local Similarity	36.0%;	Pred. No. 9.4e-06;
RESULT 950		
ID	ADI64135 standard; protein; 120 AA.	
DE	Novel human secreted and transmembrane protein PRO1056.	
PN	US2003207385-A1.	
PD	06-NOV-2003.	
PA	(GETH ) GENENTECH INC.	
Query Match	24.4%;	Score 112.5; DB 7; Length 120;
Best Local Similarity	36.0%;	Pred. No. 9.4e-06;
RESULT 951		
ID	ADI65084 standard; protein; 120 AA.	
DE	Novel human secreted and transmembrane protein PRO1056.	
PN	US2003207386-A1.	
PD	06-NOV-2003.	
PA	(GETH ) GENENTECH INC.	
Query Match	24.4%;	Score 112.5; DB 7; Length 120;
Best Local Similarity	36.0%;	Pred. No. 9.4e-06;
RESULT 952		
ID	ADI65084 standard; protein; 120 AA.	
DE	Novel human secreted and transmembrane protein PRO1056.	
PN	US2003207386-A1.	
PD	06-NOV-2003.	
PA	(GETH ) GENENTECH INC.	
Query Match	24.4%;	Score 112.5; DB 7; Length 120;
Best Local Similarity	36.0%;	Pred. No. 9.4e-06;
RESULT 953		
ID	ADI63593 standard; protein; 120 AA.	
DE	Novel human secreted and transmembrane protein PRO1056.	
PN	US2003207387-A1.	
PD	06-NOV-2003.	
PA	(GETH ) GENENTECH INC.	
Query Match	24.4%;	Score 112.5; DB 7; Length 120;
Best Local Similarity	36.0%;	Pred. No. 9.4e-06;
RESULT 954		
ID	ADH18197 standard; protein; 120 AA.	
DE	Novel human secreted and transmembrane protein PRO1056.	
PN	US2003207388-A1.	
PD	06-NOV-2003.	
PA	(GETH ) GENENTECH INC.	
Query Match	24.4%;	Score 112.5; DB 7; Length 120;
Best Local Similarity	36.0%;	Pred. No. 9.4e-06;
RESULT 955		
ID	ADH18197 standard; protein; 120 AA.	
DE	Novel human secreted and transmembrane protein PRO1056.	
PN	US2003207388-A1.	
PD	06-NOV-2003.	
PA	(GETH ) GENENTECH INC.	
Query Match	24.4%;	Score 112.5; DB 7; Length 120;
Best Local Similarity	36.0%;	Pred. No. 9.4e-06;

PN US2003194765-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 918  
ID ADE22307 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003199056-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 919  
ID ADD79531 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003203428-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 920  
ID ADE42067 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003194772-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 921  
ID ADE17884 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003199023-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 922  
ID ADD92016 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003199053-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 923  
ID ADE33479 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003194767-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 924  
ID ADE34031 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003194791-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 925  
ID ADD80083 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003207417-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 926  
ID ADD93120 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003194768-A1.

PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 927  
ID ADE19540 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003199025-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 928  
ID ADE18988 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003199026-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 929  
ID ADE43184 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003199033-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 930  
ID ADD95973 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003199059-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 931  
ID ADE22859 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003199064-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 932  
ID ADD78977 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003203429-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 933  
ID ADE26189 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003087305-A1.  
PD 08-MAY-2003.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 934  
ID ADE32927 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003194766-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 935  
ID ADE42619 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003199032-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.

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PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 899
ID ADD06818 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 900
ID ADD09536 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 901
ID ADC83065 standard; protein; 120 AA.
DE Human PRO polypeptide #50.
PN US2003059783-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 902
ID ADD41249 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 903
ID ADD52388 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 904
ID ADD53128 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 905
ID ADD53680 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 906
ID ADD55172 standard; protein; 120 AA.
DE Human PRO polypeptide #50.
PN US2003077593-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 907
ID ADD56130 standard; protein; 120 AA.
DE Human PRO polypeptide #50.
PN US2003077594-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 908
ID ADD51836 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 909
ID ADD02635 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 910
ID ADD02069 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 911
ID ADD54251 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 912
ID ADD54568 standard; protein; 120 AA.
DE Human PRO polypeptide #50.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 913
ID ADD92568 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 914
ID ADD91464 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 915
ID ADE04078 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 916
ID ADE26722 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003087304-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 917
ID ADE32375 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
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Query Match      24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 880
ID ADC59137 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein Seq ID434.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 881
ID ADC56015 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein Seq ID434.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 882
ID ADC36585 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein Seq ID434.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 883
ID ADC14499 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003082546-A1.
PD 01-MAY-2003.
Query Match      24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 884
ID ADD08031 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003068623-A1.
PD 10-APR-2003.
Query Match      24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 885
ID ADD03259 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 886
ID ADC90251 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 887
ID ADC81856 standard; protein; 120 AA.
DE Human PRO polypeptide #50.
PN US2003083461-A1.
PD 01-MAY-2003.
Query Match      24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 888
ID ADC69670 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003194770-A1.
PD 16-OCT-2003.
Query Match      24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 889
ID ADC48559 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003087358-A1.
PD 08-MAY-2003.
Query Match      24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 890
ID ADD10088 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 891
ID ADD07498 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 892
ID ADD04663 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 893
ID ADC82389 standard; protein; 120 AA.
DE Human PRO polypeptide #50.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match      24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 894
ID ADC80619 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 895
ID ADD11126 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 896
ID ADC48007 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 897
ID ADD08569 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match      24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 898
ID ADC80067 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003087358-A1.
PD 08-MAY-2003.
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Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 861  
ID ADB35103 standard; protein; 120 AA.  
DE Human PRO polypeptide SRQ ID NO 434.  
PN US2003077718-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 862  
ID ADB36207 standard; protein; 120 AA.  
DE Human PRO polypeptide SRQ ID NO 434.  
PN US2003077720-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 863  
ID ADB46602 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003082692-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 864  
ID ADC57679 standard; protein; 120 AA.  
DE Human PRO polypeptide #50.  
PN US2003027754-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 865  
ID ADC55043 standard; protein; 120 AA.  
DE Human PRO polypeptide #50.  
PN US2003045463-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 866  
ID ADC11910 standard; protein; 120 AA.  
DE Human secreted/transmembrane protein PRO1056.  
PN US2003049681-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 867  
ID ADC56332 standard; protein; 120 AA.  
DE Human PRO polypeptide #50.  
PN US2003064375-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 868  
ID ADC07387 standard; protein; 120 AA.  
DE Human secreted/transmembrane protein PRO1056.  
PN US2003068647-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 869  
ID ADC11377 standard; protein; 120 AA.  
DE Human secreted/transmembrane protein PRO1056.  
PN US2003069403-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 870  
ID ADC50475 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003092106-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.

PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 871  
ID ADC72022 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003092107-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 872  
ID ADC60001 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003092105-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 873  
ID ADC53008 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein Seq ID434.  
PN US2003087365-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 874  
ID ADC57362 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein Seq ID434.  
PN US2003087366-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 875  
ID ADC60553 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003087367-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 876  
ID ADC51028 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003087361-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 877  
ID ADC65555 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003087362-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 878  
ID ADC54653 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein Seq ID434.  
PN US2003087363-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 879  
ID ADC53614 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein Seq ID434.  
PN US2003087364-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.

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DE Human secreted/transmembrane protein PRO1056.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 843
ID ADA67055 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 844
ID ADB22916 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US200307711-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 845
ID ADB23689 standard; protein; 120 AA.
DE Human PRO polypeptide SEQ ID NO 434.
PN US200307712-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 846
ID ADA92411 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 847
ID ADB15474 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 848
ID ADB38726 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 849
ID ADB96207 standard; protein; 120 AA.
DE Human PRO polypeptide #50.
PN US2003054403-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 850
ID ADB38174 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 851
ID ADB66646 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 852
ID ADB89726 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 853
ID ADB90458 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 854
ID ADB39559 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 855
ID ADB47182 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 856
ID ADB86789 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 857
ID ADB77394 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 858
ID ADB34551 standard; protein; 120 AA.
DE Human PRO polypeptide SEQ ID NO 434.
PN US200307717-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 859
ID ADB35655 standard; protein; 120 AA.
DE Human PRO polypeptide SEQ ID NO 434.
PN US200307719-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 860
ID ADB33999 standard; protein; 120 AA.
DE Human PRO polypeptide SEQ ID NO 434.
PN US200307716-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
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DE Human PRO polypeptide #217.  
PN US2003082759-A1.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 824  
ID ADB26327 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003082760-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 825  
ID ADB21812 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003082765-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 826  
ID ADA77591 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003068797-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 827  
ID ADB18331 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003077710-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 828  
ID ADA87014 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003082709-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 829  
ID ADA88117 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003082700-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 830  
ID ADA46505 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003054516-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 831  
ID ADB28535 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003082699-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 832  
ID ADB29087 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.

PN US2003082706-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 833  
ID ABO53155 standard; protein; 120 AA.  
DE Human secreted/transmembrane protein PRO1056.  
PN US2003044806-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 834  
ID ADA77039 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003059909-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 835  
ID ADA22322 standard; protein; 120 AA.  
DE Human secreted/transmembrane polypeptide PRO1056.  
PN US2003040473-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 836  
ID ADA88669 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003073213-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 837  
ID ADA97674 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003082686-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 838  
ID ADB27431 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003022239-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 839  
ID ADB22364 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003087344-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 840  
ID ABO22525 standard; protein; 120 AA.  
DE Human secreted/transmembrane protein PRO1056.  
PN US2003017982-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 841  
ID ADA06488 standard; protein; 120 AA.  
DE Human secreted/transmembrane PRO polypeptide #50.  
PN US2003049638-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 842  
ID ADA39181 standard; protein; 120 AA.

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Query Match      24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 805
ID ADA82317 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 806
ID ADA75280 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 807
ID ADA85358 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 808
ID ADA84806 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 809
ID ADB30062 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 810
ID ADA80590 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 811
ID ADA75832 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 812
ID ADA38640 standard; protein; 120 AA.
DE Human secreted/transmembrane protein PRO1056.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match      24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 813
ID ADA47057 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 814
ID ADB25353 standard; protein; 120 AA.
DE Human PRO polypeptide SEQ ID NO 434.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 815
ID ADA93529 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 816
ID ADB26879 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 817
ID ADB31166 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 818
ID ADA92761 standard; protein; 120 AA.
DE Human secreted/transmembrane protein PRO1056.
PN US2003060407-A1.
PD 27-MAR-2003.
Query Match      24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 819
ID ADA61094 standard; protein; 120 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 820
ID ADB24241 standard; protein; 120 AA.
DE Human PRO polypeptide SEQ ID NO 434.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 821
ID ADA96570 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 822
ID ADA81142 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 823
ID ADA96018 standard; protein; 120 AA.
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ID ADA67607 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 787
ID ADB14922 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 796
ID ADB14922 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 797
ID ADB18883 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 798
ID ADA94098 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 799
ID ADB19994 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 800
ID ADB13306 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 801
ID ABO43365 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 802
ID ADA94415 standard; protein; 120 AA.
DE Human secreted/transmembrane protein PRO1056.
PN US2003059832-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 803
ID ADA74560 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 804
ID ADB24793 standard; protein; 120 AA.
DE Human PRO polypeptide SEQ ID NO 434.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 805
ID ADA7565 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 792
ID ADA87565 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 793
ID ADB16767 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 794
ID ADA27835 standard; protein; 120 AA.
DE Human secreted/transmembrane protein PRO1056.
PN US2003054359-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 795
ID ADA91859 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003082694-A1.
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DE Novel human secreted or transmembrane protein PRO826.  
PN US2003027985-A1.  
PD 06-FEB-2003.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 768  
ID ABU67062 standard; protein; 120 AA.  
DE Human secreted/transmembrane, PRO, protein SEQ ID 434.  
PN US2003032155-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 769  
ID ABU92158 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003017476-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 770  
ID ABU10864 standard; protein; 120 AA.  
DE Human PRO polypeptide #50.  
PN US2002123463-A1.  
PD 05-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 771  
ID ABU81616 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2002177164-A1.  
PD 28-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 772  
ID ABO34069 standard; protein; 120 AA.  
DE Human secreted and transmembrane polypeptide.  
PN US2003017981-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 773  
ID ABO34069 standard; protein; 120 AA.  
DE Human secreted and transmembrane polypeptide.  
PN US2003017981-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 774  
ID ADA45953 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003022328-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 775  
ID ADA76384 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003073212-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 776  
ID ADA19034 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003054517-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 777  
ID ADA61657 standard; protein; 120 AA.  
DE Homo sapiens.  
PN US2003049816-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 778  
ID ADB19442 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003068796-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 779  
ID ADB27983 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003082704-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 780  
ID ADA86462 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003082711-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 781  
ID ADB16026 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003087350-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 782  
ID ADA37710 standard; protein; 120 AA.  
DE Human secreted/transmembrane protein PRO1056.  
PN US2003008297-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 783  
ID ADA47812 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003073215-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 784  
ID ADA21396 standard; protein; 120 AA.  
DE Human secreted/transmembrane polypeptide PRO1056.  
PN US2003054404-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 785  
ID ADA10183 standard; protein; 120 AA.  
DE Human secreted/transmembrane protein, PRO1056.  
PN US2003059831-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 786

PD 04-DEC-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 96;  
Best Local Similarity 36.0%; Pred. No. 7.1e-06;  
RESULT 749  
ID AAY66680 standard; protein; 120 AA.  
DE Membrane-bound protein PRO1056.  
PN WO9963088-A2.  
PD 09-DEC-1999.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 3; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 750  
ID AAU12388 standard; protein; 120 AA.  
DE Human PRO1056 polypeptide sequence.  
PN WO200140466-A2.  
PD 07-JUN-2001.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 4; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 751  
ID AAB65203 standard; protein; 120 AA.  
DE Human PRO1056 (UNQ521) protein sequence SEQ ID NO:199.  
PN WO200073454-A1.  
PD 07-DEC-2000.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 4; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 752  
ID ABUS8018 standard; protein; 120 AA.  
DE Human PRO polypeptide #50.  
PN US2003027453-A1.  
PD 06-FEB-2003.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 753  
ID ABUS9096 standard; protein; 120 AA.  
DE Novel human secreted or transmembrane protein PRO1056.  
PN US2002132252-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 754  
ID ABUS8608 standard; protein; 120 AA.  
DE Human secreted/transmembrane protein PRO1056.  
PN US2003032023-A1.  
PD 13-FEB-2003.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 755  
ID ABO17832 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003032156-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 756  
ID ABUS60527 standard; protein; 120 AA.  
DE Human secreted/transmembrane protein, #77.  
PN US2002160384-A1.  
PD 31-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 757  
ID ABUI3909 standard; protein; 120 AA.  
DE Human PRO1056 polypeptide.  
PN US2002103125-A1.  
PD 01-AUG-2002.  
PA (GETH ) GENENTECH LTD.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 758  
ID ABUS1086 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003004311-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 759  
ID ABU72494 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003003531-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 760  
ID ABU66786 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003036180-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 761  
ID ABUS9867 standard; protein; 120 AA.  
DE Novel secreted and transmembrane protein PRO1056.  
PN US2003017563-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 762  
ID ABUS9243 standard; protein; 120 AA.  
DE Human secreted/transmembrane protein, #77.  
PN US2003027162-A1.  
PD 06-FEB-2003.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 763  
ID ABO25940 standard; protein; 120 AA.  
DE Human PRO1056 polypeptide.  
PN US2002127576-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 764  
ID ABO25057 standard; protein; 120 AA.  
DE Human secreted/transmembrane protein (PRO) #217.  
PN US2003036179-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 765  
ID ABUS8949 standard; protein; 120 AA.  
DE Human secreted/transmembrane protein, #77.  
PN US2002142961-A1.  
PD 03-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 766  
ID ABU92327 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003022187-A1.  
PD 30-JAN-2003.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9.4e-06;  
RESULT 767  
ID ABUS9392 standard; protein; 120 AA.

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PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC. 24.6%; Score 113.5; DB 4; Length 155;
Best Local Similarity 34.2%; Pred. No. 9.8e-06;
RESULT 738
ID AAW51104 standard; protein; 95 AA.
DE A human phospholemmann-like protein.
PN WO9814572-A1.
PD 09-APR-1998.
PA (INCY-) INCYTE PHARM INC. 24.4%; Score 112.5; DB 2; Length 95;
Best Local Similarity 36.0%; Pred. No. 7e-06;
RESULT 739
ID AAU14575 standard; protein; 95 AA.
DE Human novel protein #446.
PN WO200155437-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC. 24.4%; Score 112.5; DB 4; Length 95;
Best Local Similarity 36.0%; Pred. No. 7e-06;
RESULT 740
ID ABUS2798 standard; protein; 95 AA.
DE Human signal transduction-associated protein from DKF2phfbr2_82117.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT. 24.4%; Score 112.5; DB 4; Length 95;
Best Local Similarity 36.0%; Pred. No. 7e-06;
RESULT 741
ID ADH80893 standard; protein; 95 AA.
DE Human polypeptide #210.
PN US2003232054-A1.
PD 18-DEC-2003.
PA (TANG/) TANG Y T.
PA (LIUC/) LIU C.
PA (ASUN/) ASUNDI V.
PA (CHEN/) CHEN R.
PA (QIAN/) QIAN X B.
PA (WANG/) WANG Z W.
PA (WEHR/) WEHRMAN T.
PA (ZHAN/) ZHANG J.
PA (ZHOU/) ZHOU P.
PA (CAOY/) CAO Y.
PA (DRMA/) DRMANAC R T.
Query Match 24.4%; Score 112.5; DB 8; Length 95;
Best Local Similarity 36.0%; Pred. No. 7e-06;
RESULT 742
ID ABM81305 standard; protein; 95 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO82051, SEQ:3370.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH-) GENENTECH INC. 24.4%; Score 112.5; DB 8; Length 95;
Best Local Similarity 36.0%; Pred. No. 7e-06;
RESULT 743
ID ABE24249 standard; protein; 95 AA.
DE Novel human protein amino acid sequence - SEQ ID 918.
PN US2005266423-A1.
PD 01-DEC-2005.
PA (NUVE-) NUVELO INC. 24.4%; Score 112.5; DB 10; Length 95;
Best Local Similarity 36.0%; Pred. No. 7e-06;
RESULT 744
ID AAW74882 standard; protein; 96 AA.
DE Human secreted protein encoded by gene 154 clone HE6FL83.
PN WO9839448-A2.
PD 11-SEP-1998.
PA (HUMA-) HUMAN GENOME SCI INC. 24.4%; Score 112.5; DB 2; Length 96;
Best Local Similarity 36.0%; Pred. No. 7.1e-06;
RESULT 745
ID ASG95333 standard; protein; 96 AA.
DE Human novel secreted protein #154.
PN US2003225248-A1.

PN US6420526-B1.
PD 16-JUL-2002.
PA (HUMA-) HUMAN GENOME SCI INC. 24.4%; Score 112.5; DB 5; Length 96;
Query Match 36.0%; Pred. No. 7.1e-06;
Best Local Similarity 36.0%; Pred. No. 7.1e-06;
RESULT 746
ID ABQ34527 standard; protein; 96 AA.
DE Region of human secreted protein encoded by cDNA sequence #154.
PN US2003049618-A1.
PD 13-MAR-2003.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (CART/) CARTER K C.
PA (BEDN/) BEDNARIK D P.
PA (ENDR/) ENDRESS G A.
PA (YUGG/) YU G.
PA (NIJJ/) NI J.
PA (FENG/) FENG P.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (DUAN/) DUAN D R.
PA (HUJJ/) HU J.
PA (FLOR/) FLORENCE K A.
PA (OLSE/) OLSEN H S.
PA (FISC/) FISCHER C L.
PA (EBNE/) EBNER R.
PA (BREW/) BREWER L A.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (LAPL/) LAFLEUR D W.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
Query Match 24.4%; Score 112.5; DB 6; Length 96;
Best Local Similarity 36.0%; Pred. No. 7.1e-06;
RESULT 747
ID ADI23188 standard; protein; 96 AA.
DE Novel human secreted protein seq id 473.
PN US2003175858-A1.
PD 18-SEP-2003.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (CART/) CARTER K C.
PA (BEDN/) BEDNARIK D P.
PA (ENDR/) ENDRESS G A.
PA (YUGG/) YU G.
PA (NIJJ/) NI J.
PA (FENG/) FENG P.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (DUAN/) DUAN D R.
PA (HUJJ/) HU J.
PA (FLOR/) FLORENCE K A.
PA (OLSE/) OLSEN H S.
PA (FISC/) FISCHER C L.
PA (EBNE/) EBNER R.
PA (BREW/) BREWER L A.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (LAPL/) LAFLEUR D W.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
Query Match 24.4%; Score 112.5; DB 7; Length 96;
Best Local Similarity 36.0%; Pred. No. 7.1e-06;
RESULT 748
ID ADH74190 standard; protein; 96 AA.
DE Human secreted protein #154.
PN US2003225248-A1.
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PA (EDWA/) EDWARDS J D M.  
PA (DUCL/) DUCLET A.  
PA (BOUG/) BOUGUELERET L.  
Query Match 28.0%; Score 129; DB 9; Length 92;  
Best Local Similarity 41.3%; Pred. No. 5.4e-08;  
RESULT 725  
ID AAW75106 standard; protein; 93 AA.  
DE Human secreted protein encoded by gene 50 clone HUSDZ57.  
PN WO9839446-A2.  
PD 11-SEP-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 28.0%; Score 129; DB 2; Length 93;  
Best Local Similarity 41.3%; Pred. No. 5.5e-08;  
RESULT 726  
ID ABO01982 standard; protein; 93 AA.  
DE Novel human secreted protein #50.  
PN US2003027132-A1.  
PD 06-FEB-2003.  
PA (RUBE/) RUBEN S M.  
PA (ROSE/) ROSEN C A.  
PA (FISC/) FISCHER C L.  
PA (SOPP/) SOPPET D R.  
PA (CART/) CARTER K C.  
PA (BEDN/) BEDNARIK D R.  
PA (ENDR/) ENDRESS G A.  
PA (YUGG/) YU G.  
PA (NIJ/) NI J.  
PA (FENG/) FENG P.  
PA (YOUN/) YOUNG P E.  
PA (GREE/) GREENE J M.  
PA (FERR/) FERRIE A M.  
PA (DUAN/) DUAN R.  
PA (HUJ/) HU J.  
PA (FLOR/) FLORENCE K A.  
PA (OLSE/) OLSEN H S.  
PA (EBNE/) EBNER R.  
PA (BREW/) BREWER L A.  
PA (SHIY/) SHI Y.  
Query Match 28.0%; Score 129; DB 6; Length 93;  
Best Local Similarity 41.3%; Pred. No. 5.5e-08;  
RESULT 727  
ID AD212383 standard; protein; 93 AA.  
DE Human secreted protein sequence encoded by gene 50 SEQ ID NO:183.  
PN US6878687-B1.  
PD 12-APR-2005.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 28.0%; Score 129; DB 9; Length 93;  
Best Local Similarity 41.3%; Pred. No. 5.5e-08;  
RESULT 728  
ID ABO02067 standard; protein; 70 AA.  
DE Novel human secreted protein associated protein fragment #12.  
PN US2003027132-A1.  
PD 06-FEB-2003.  
PA (RUBE/) RUBEN S M.  
PA (ROSE/) ROSEN C A.  
PA (FISC/) FISCHER C L.  
PA (SOPP/) SOPPET D R.  
PA (CART/) CARTER K C.  
PA (BEDN/) BEDNARIK D R.  
PA (ENDR/) ENDRESS G A.  
PA (YUGG/) YU G.  
PA (NIJ/) NI J.  
PA (FENG/) FENG P.  
PA (YOUN/) YOUNG P E.  
PA (GREE/) GREENE J M.  
PA (FERR/) FERRIE A M.  
PA (DUAN/) DUAN R.  
PA (HUJ/) HU J.  
PA (FLOR/) FLORENCE K A.  
PA (OLSE/) OLSEN H S.  
PA (EBNE/) EBNER R.  
PA (BREW/) BREWER L A.  
PA (SHIY/) SHI Y.

Query Match 26.2%; Score 121; DB 6; Length 70;  
Best Local Similarity 44.9%; Pred. No. 3.9e-07;  
RESULT 729  
ID AD212469 standard; protein; 70 AA.  
DE Human gene 50 secreted protein related sequence SEQ ID NO:269.  
PN US6878687-B1.  
PD 12-APR-2005.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 26.2%; Score 121; DB 9; Length 70;  
Best Local Similarity 44.9%; Pred. No. 3.9e-07;  
RESULT 730  
ID AAV12377 standard; protein; 63 AA.  
DE Human 5' EST secreted protein SEQ ID NO:408.  
PN WO9906548-A2.  
PD 11-FEB-1999.  
PA (GEST/) GENSET.  
Query Match 24.7%; Score 114; DB 2; Length 63;  
Best Local Similarity 43.1%; Pred. No. 2.7e-06;  
RESULT 731  
ID ADE58523 standard; protein; 92 AA.  
DE Rat Protein O08589, SEQ ID NO 4398.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO/) GEN HOSPITAL CORP.  
PA (FARB/) BAYER AG.  
Query Match 24.7%; Score 114; DB 7; Length 92;  
Best Local Similarity 31.6%; Pred. No. 4.3e-06;  
RESULT 732  
ID ADE58519 standard; protein; 92 AA.  
DE Rat Protein O08589, SEQ ID NO 4394.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO/) GEN HOSPITAL CORP.  
PA (FARB/) BAYER AG.  
Query Match 24.7%; Score 114; DB 7; Length 92;  
Best Local Similarity 31.6%; Pred. No. 4.3e-06;  
RESULT 733  
ID ADE83503 standard; protein; 92 AA.  
DE Rat Protein O08589, SEQ ID NO 11099.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO/) GEN HOSPITAL CORP.  
PA (FARB/) BAYER AG.  
Query Match 24.7%; Score 114; DB 7; Length 92;  
Best Local Similarity 31.6%; Pred. No. 4.3e-06;  
RESULT 734  
ID AAM38777 standard; protein; 138 AA.  
DE Human polypeptide SEQ ID NO 1922.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 24.6%; Score 113.5; DB 4; Length 138;  
Best Local Similarity 34.2%; Pred. No. 8.4e-06;  
RESULT 735  
ID AAU14339 standard; protein; 138 AA.  
DE Human novel protein #210.  
PN WO200155437-A2.  
PD 02-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 24.6%; Score 113.5; DB 4; Length 138;  
Best Local Similarity 34.2%; Pred. No. 8.4e-06;  
RESULT 736  
ID AEE23777 standard; protein; 138 AA.  
DE Novel human protein amino acid sequence - SEQ ID 446.  
PN US2005266423-A1.  
PD 01-DEC-2005.  
PA (NUVE-) NUVELO INC.  
Query Match 24.6%; Score 113.5; DB 10; Length 138;  
Best Local Similarity 34.2%; Pred. No. 8.4e-06;  
RESULT 737  
ID AAM40563 standard; protein; 155 AA.  
DE Human polypeptide SEQ ID NO 5494.  
PN WO200153312-A1.



PD 11-SEP-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 28.0%; Score 129; DB 2; Length 92;  
Best Local Similarity 41.3%; Pred. No. 5.4e-08;  
RESULT 710  
ID AAY24749 standard; protein; 92 AA.  
DE Human phospholemmann homologue protein.  
PN US5919655-A.  
PD 06-JUL-1999.  
PA (INCY-) INCYTE PHARM INC.  
Query Match 28.0%; Score 129; DB 2; Length 92;  
Best Local Similarity 41.3%; Pred. No. 5.4e-08;  
RESULT 711  
ID AAY59689 standard; protein; 92 AA.  
DE Secreted protein 26-44-1-B5-CL3\_1.  
PN WO9940189-A2.  
PD 12-AUG-1999.  
PA (GEST ) GENSET.  
Query Match 28.0%; Score 129; DB 2; Length 92;  
Best Local Similarity 41.3%; Pred. No. 5.4e-08;  
RESULT 712  
ID AAY48331 standard; protein; 92 AA.  
DE Human prostate cancer-associated protein 28.  
PN DE19811194-A1.  
PD 16-SEP-1999.  
PA (META-) METAGEN GES GENOMFORSCHUNG MEH.  
Query Match 28.0%; Score 129; DB 2; Length 92;  
Best Local Similarity 41.3%; Pred. No. 5.4e-08;  
RESULT 713  
ID AAW92960 standard; protein; 92 AA.  
DE Human PLM protein.  
PN WO9905276-A1.  
PD 04-FEB-1999.  
PA (ZYMO ) ZYMOGENETICS INC.  
Query Match 28.0%; Score 129; DB 2; Length 92;  
Best Local Similarity 41.3%; Pred. No. 5.4e-08;  
RESULT 714  
ID ABB97244 standard; protein; 92 AA.  
DE Novel human protein SEQ ID NO: 512.  
PN WO200222660-A2.  
PD 21-MAR-2002.  
PA (HYSE-) HYSQ INC.  
Query Match 28.0%; Score 129; DB 5; Length 92;  
Best Local Similarity 41.3%; Pred. No. 5.4e-08;  
RESULT 715  
ID ABO2037 standard; protein; 92 AA.  
DE Novel human secreted protein #105.  
PN US2003027132-A1.  
PD 06-FEB-2003.  
PA (RUBE/) RUBEN S M.  
PA (ROSE/) ROSEN C A.  
PA (FISC/) FISCHER C L.  
PA (SOPP/) SOPPET D R.  
PA (CART/) CARTER K C.  
PA (BEDN/) BEDNARIK D R.  
PA (ENDR/) ENDRESS G A.  
PA (YUGG/) YU G.  
PA (NIJJ/) NI J.  
PA (FENG/) FENG P.  
PA (YOUN/) YOUNG P E.  
PA (GREE/) GREENE J M.  
PA (FERR/) FERRIE A M.  
PA (DUAN/) DUAN R.  
PA (HUJU/) HU J.  
PA (FLOR/) FLORENCE K A.  
PA (OLSE/) OLSEN H S.  
PA (EBNE/) EBNER R.  
PA (BREW/) BREWER L A.  
PA (SHIY/) SHI Y.  
Query Match 28.0%; Score 129; DB 6; Length 92;  
Best Local Similarity 41.3%; Pred. No. 5.4e-08;  
RESULT 716  
ID ADE58521 standard; protein; 92 AA.

DE Human Protein O00168, SEQ ID NO 4396.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 28.0%; Score 129; DB 7; Length 92;  
Best Local Similarity 41.3%; Pred. No. 5.4e-08;  
RESULT 717  
ID ADE58525 standard; protein; 92 AA.  
DE Human Protein O00168, SEQ ID NO 4400.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 28.0%; Score 129; DB 7; Length 92;  
Best Local Similarity 41.3%; Pred. No. 5.4e-08;  
RESULT 718  
ID ADE83505 standard; protein; 92 AA.  
DE Human Protein O00168, SEQ ID NO 11101.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 28.0%; Score 129; DB 7; Length 92;  
Best Local Similarity 41.3%; Pred. No. 5.4e-08;  
RESULT 719  
ID ADJ69464 standard; protein; 92 AA.  
DE Human heat mitochondrial protein as a therapeutic target SeqID1270.  
PN WO2003087768-A2.  
PD 23-OCT-2003.  
PA (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES.  
Query Match 28.0%; Score 129; DB 7; Length 92;  
Best Local Similarity 41.3%; Pred. No. 5.4e-08;  
RESULT 720  
ID ADM77839 standard; protein; 92 AA.  
DE Human protein #36.  
PN US2003162176-A1.  
PD 28-AUG-2003.  
PA (EDWA/) EDWARDS J D M.  
PA (DUCL/) DUCLETT A.  
PA (BOUG/) BOUGUELERET L.  
Query Match 28.0%; Score 129; DB 7; Length 92;  
Best Local Similarity 41.3%; Pred. No. 5.4e-08;  
RESULT 721  
ID ADN05844 standard; protein; 92 AA.  
DE Antipsoriatic protein sequence #1085.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 28.0%; Score 129; DB 8; Length 92;  
Best Local Similarity 41.3%; Pred. No. 5.4e-08;  
RESULT 722  
ID ADP19520 standard; protein; 92 AA.  
DE Human secreted polypeptide #371.  
PN US2004110939-A1.  
PD 10-JUN-2004.  
PA (GEST ) GENSET SA.  
Query Match 28.0%; Score 129; DB 8; Length 92;  
Best Local Similarity 41.3%; Pred. No. 5.4e-08;  
RESULT 723  
ID ADZ12438 standard; protein; 92 AA.  
DE Human secreted protein sequence encoded by gene 50 SEQ ID NO:238.  
PN US6878687-B1.  
PD 12-APR-2005.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 28.0%; Score 129; DB 9; Length 92;  
Best Local Similarity 41.3%; Pred. No. 5.4e-08;  
RESULT 724  
ID ADZ89299 standard; protein; 92 AA.  
DE Secreted protein encoded by extended EST cDNA #36.  
PN US2005106599-A1.  
PD 19-MAY-2005.

DE Novel human polypeptide NOV13b.  
PN US2004018555-A1.  
PD 29-JAN-2004.  
PA (ANDE/) ANDERSON D W.  
PA (ZERH/) ZERHUSEN B D.  
PA (LILL/) LI L.  
PA (ZHON/) ZHONG M.  
PA (CASM/) CASMAN S J.  
PA (GERL/) GERLACH V.  
PA (SHIM/) SHIMKETS R A.  
PA (GORM/) GORMAN L.  
PA (PENA/) PENA C E A.  
PA (KEKU/) KEKUDA R.  
PA (PATT/) PATTURAJAN M.  
PA (SPYT/) SPYTEK K A.  
PA (LEIT/) LEITE M W.  
PA (MACT/) MACDOUGALL J R.  
PA (TAUP/) TAUPIER R J.  
PA (GUOX/) GUO X S.  
PA (MILL/) MILLER C E.  
PA (SHEN/) SHENOY S G.  
PA (HJAL/) HJALT T.  
PA (VOSS/) VOSS E Z.  
PA (BOLD/) BOLDOG F L.  
PA (MALY/) MALYANKAR U M.  
PA (PADI/) PADIGARU M.  
PA (JIWW/) JI W.  
PA (SMIT/) SMITHSON G.  
PA (EDIN/) EDINGER S R.  
PA (MILL/) MILLET I.  
PA (ELLE/) ELLERMAN K.  
Query Match 46.5%; Score 214.5; DB 8; Length 116;  
Best Local Similarity 54.5%; Pred. No. 1.1e-18;  
RESULT 699  
ID ABJ19333 standard; protein; 86 AA.  
DE NOVX related protein SEQ ID NO 32.  
PN WO200299062-A2.  
PD 12-DEC-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 45.4%; Score 209.5; DB 6; Length 86;  
Best Local Similarity 54.0%; Pred. No. 3.1e-18;  
RESULT 700  
ID AD041666 standard; protein; 86 AA.  
DE Novel human polypeptide NOV13a.  
PN US2004018555-A1.  
PD 29-JAN-2004.  
PA (ANDE/) ANDERSON D W.  
PA (ZERH/) ZERHUSEN B D.  
PA (LILL/) LI L.  
PA (ZHON/) ZHONG M.  
PA (CASM/) CASMAN S J.  
PA (GERL/) GERLACH V.  
PA (SHIM/) SHIMKETS R A.  
PA (GORM/) GORMAN L.  
PA (PENA/) PENA C E A.  
PA (KEKU/) KEKUDA R.  
PA (PATT/) PATTURAJAN M.  
PA (SPYT/) SPYTEK K A.  
PA (LEIT/) LEITE M W.  
PA (MACT/) MACDOUGALL J R.  
PA (TAUP/) TAUPIER R J.  
PA (GUOX/) GUO X S.  
PA (MILL/) MILLER C E.  
PA (SHEN/) SHENOY S G.  
PA (HJAL/) HJALT T.  
PA (VOSS/) VOSS E Z.  
PA (BOLD/) BOLDOG F L.  
PA (MALY/) MALYANKAR U M.  
PA (PADI/) PADIGARU M.  
PA (JIWW/) JI W.  
PA (SMIT/) SMITHSON G.  
PA (EDIN/) EDINGER S R.  
PA (MILL/) MILLET I.  
PA (ELLE/) ELLERMAN K.  
Query Match 45.4%; Score 209.5; DB 8; Length 111;  
Best Local Similarity 42.1%; Pred. No. 1.2e-15;  
RESULT 705  
ID ADI36717 standard; protein; 111 AA.  
DE Human PLML #1.  
PN US2003225014-A1.  
PD 04-DEC-2003.  
PA (ISIS-) ISIS PHARM INC.  
Query Match 38.1%; Score 175.5; DB 8; Length 111;  
Best Local Similarity 41.2%; Pred. No. 8.8e-14;  
RESULT 706  
ID ADZ69595 standard; protein; 111 AA.  
DE Human phospholeman-like protein (PLML) SEQ ID NO:3.  
PN US2005101558-A1.  
PD 12-MAY-2005.  
PA (WART/) WAIT A T.  
Query Match 38.1%; Score 175.5; DB 9; Length 111;  
Best Local Similarity 41.2%; Pred. No. 8.8e-14;  
RESULT 707  
ID ABG75941 standard; protein; 67 AA.  
DE Transporters and ion channels protein 23, TRICH-23.  
PN WO2003016493-A2.  
PD 27-FEB-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 32.5%; Score 150; DB 6; Length 67;  
Best Local Similarity 56.6%; Pred. No. 7.8e-11;  
RESULT 708  
ID ABU52799 standard; protein; 83 AA.  
DE Human signal transduction-associated DKPzphfbr2\_82i17 homologue.  
PN WO200112659-A2.  
PD 22-FEB-2001.  
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.  
Query Match 28.0%; Score 129; DB 4; Length 83;  
Best Local Similarity 41.3%; Pred. No. 4.7e-08;  
RESULT 709  
ID AAW75161 standard; protein; 92 AA.  
DE Human secreted protein encoded by gene 50 clone HHSD257.  
PN WO9839446-A2.

PA (EDIN/) EDINGER S R.  
PA (MILL/) MILLET I.  
PA (ELLE/) ELLERMAN K.  
Query Match 45.4%; Score 209.5; DB 8; Length 86;  
Best Local Similarity 54.0%; Pred. No. 3.1e-18;  
RESULT 701  
ID ABR47468 standard; protein; 113 AA.  
DE Breast cancer associated protein sequence SEQ ID NO:168.  
PN WO2003004989-A2.  
PD 16-JAN-2003.  
PA (MILL-) MILLENIUM PHARM INC.  
Query Match 41.5%; Score 191.5; DB 6; Length 113;  
Best Local Similarity 42.1%; Pred. No. 8.4e-16;  
RESULT 702  
ID ADB75318 standard; protein; 113 AA.  
DE Prostate cancer marker protein.  
PN WO2003009814-A2.  
PD 06-FEB-2003.  
PA (MILL-) MILLENIUM PHARM INC.  
Query Match 41.5%; Score 191.5; DB 7; Length 113;  
Best Local Similarity 42.1%; Pred. No. 8.4e-16;  
RESULT 703  
ID ADN40039 standard; protein; 113 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C409.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 41.5%; Score 191.5; DB 7; Length 113;  
Best Local Similarity 42.1%; Pred. No. 8.4e-16;  
RESULT 704  
ID AAB53415 standard; protein; 150 AA.  
DE Human colon cancer antigen protein sequence SEQ ID NO:955.  
PN WO200055351-A1.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 41.5%; Score 191.5; DB 3; Length 150;  
Best Local Similarity 42.1%; Pred. No. 1.2e-15;  
RESULT 705  
ID ADI36717 standard; protein; 111 AA.  
DE Human PLML #1.  
PN US2003225014-A1.  
PD 04-DEC-2003.  
PA (ISIS-) ISIS PHARM INC.  
Query Match 38.1%; Score 175.5; DB 8; Length 111;  
Best Local Similarity 41.2%; Pred. No. 8.8e-14;  
RESULT 706  
ID ADZ69595 standard; protein; 111 AA.  
DE Human phospholeman-like protein (PLML) SEQ ID NO:3.  
PN US2005101558-A1.  
PD 12-MAY-2005.  
PA (WART/) WAIT A T.  
Query Match 38.1%; Score 175.5; DB 9; Length 111;  
Best Local Similarity 41.2%; Pred. No. 8.8e-14;  
RESULT 707  
ID ABG75941 standard; protein; 67 AA.  
DE Transporters and ion channels protein 23, TRICH-23.  
PN WO2003016493-A2.  
PD 27-FEB-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 32.5%; Score 150; DB 6; Length 67;  
Best Local Similarity 56.6%; Pred. No. 7.8e-11;  
RESULT 708  
ID ABU52799 standard; protein; 83 AA.  
DE Human signal transduction-associated DKPzphfbr2\_82i17 homologue.  
PN WO200112659-A2.  
PD 22-FEB-2001.  
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.  
Query Match 28.0%; Score 129; DB 4; Length 83;  
Best Local Similarity 41.3%; Pred. No. 4.7e-08;  
RESULT 709  
ID AAW75161 standard; protein; 92 AA.  
DE Human secreted protein encoded by gene 50 clone HHSD257.  
PN WO9839446-A2.

DE Mouse Mat-8 polypeptide.  
PN WO9605322-A1.  
PD 22-FEB-1996.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (HARD ) HARVARD COLLEGE.  
Query Match 52.4%; Score 241.5; DB 2; Length 88;  
Best Local Similarity 57.8%; Pred. No. 2.8e-22;  
RESULT 681  
ID AAR90990 standard; protein; 87 AA.  
DE Human Mat-8 polypeptide.  
PN WO9605322-A1.  
PD 22-FEB-1996.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (HARD ) HARVARD COLLEGE.  
Query Match 46.5%; Score 214.5; DB 2; Length 87;  
Best Local Similarity 54.5%; Pred. No. 7.3e-19;  
RESULT 682  
ID AAY48304 standard; protein; 87 AA.  
DE Human prostate cancer-associated protein 1.  
PN DE19811194-A1.  
PD 16-SEP-1999.  
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.  
Query Match 46.5%; Score 214.5; DB 2; Length 87;  
Best Local Similarity 54.5%; Pred. No. 7.3e-19;  
RESULT 683  
ID AAW92959 standard; protein; 87 AA.  
DE Human MAT-8 protein.  
PN WO9905276-A1.  
PD 04-FEB-1999.  
PA (ZYMO ) ZYMOGENETICS INC.  
Query Match 46.5%; Score 214.5; DB 2; Length 87;  
Best Local Similarity 54.5%; Pred. No. 7.3e-19;  
RESULT 684  
ID AAM23962 standard; protein; 87 AA.  
DE Human EST encoded protein SEQ ID NO: 1487.  
PN WO200154477-A2.  
PD 02-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 46.5%; Score 214.5; DB 4; Length 87;  
Best Local Similarity 54.5%; Pred. No. 7.3e-19;  
RESULT 685  
ID ABJ37036 standard; protein; 87 AA.  
DE Human breast cancer / ovarian cancer related protein #12.  
PN WO2003000012-A2.  
PD 03-JAN-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 46.5%; Score 214.5; DB 6; Length 87;  
Best Local Similarity 54.5%; Pred. No. 7.3e-19;  
RESULT 686  
ID ABR47467 standard; protein; 87 AA.  
DE Breast cancer associated protein sequence SEQ ID NO:166.  
PN WO2003004989-A2.  
PD 16-JAN-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 46.5%; Score 214.5; DB 6; Length 87;  
Best Local Similarity 54.5%; Pred. No. 7.3e-19;  
RESULT 687  
ID ABP75985 standard; protein; 87 AA.  
DE Human GENSET protein SEQ ID 192.  
PN WO200283898-A1.  
PD 24-OCT-2002.  
PA (GEST ) GENSET.  
Query Match 46.5%; Score 214.5; DB 6; Length 87;  
Best Local Similarity 54.5%; Pred. No. 7.3e-19;  
RESULT 688  
ID ABP76150 standard; protein; 87 AA.  
DE Human GENSET protein SEQ ID 476.  
PN WO200283898-A1.  
PD 24-OCT-2002.  
PA (GEST ) GENSET.  
Query Match 46.5%; Score 214.5; DB 6; Length 87;  
Best Local Similarity 54.5%; Pred. No. 7.3e-19;  
RESULT 689  
ID ADO41668 standard; protein; 116 AA.  
DE ADB75316 standard; protein; 87 AA.  
DE Prostate cancer marker protein.  
PN WO2003009814-A2.  
PD 06-FEB-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 46.5%; Score 214.5; DB 7; Length 87;  
Best Local Similarity 54.5%; Pred. No. 7.3e-19;  
RESULT 690  
ID ADM40040 standard; protein; 87 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C410.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 46.5%; Score 214.5; DB 7; Length 87;  
Best Local Similarity 54.5%; Pred. No. 7.3e-19;  
RESULT 691  
ID ADI36718 standard; protein; 87 AA.  
DE Human PLML #2.  
PN US2003225014-A1.  
PD 04-DEC-2003.  
PA (ISIS-) ISIS PHARM INC.  
Query Match 46.5%; Score 214.5; DB 8; Length 87;  
Best Local Similarity 54.5%; Pred. No. 7.3e-19;  
RESULT 692  
ID ADK70447 standard; protein; 87 AA.  
DE Respiratory disease differentially expressed protein #13.  
PN WO2003101283-A2.  
PD 11-DEC-2003.  
PA (INCY-) INCYTE CORP.  
Query Match 46.5%; Score 214.5; DB 8; Length 87;  
Best Local Similarity 54.5%; Pred. No. 7.3e-19;  
RESULT 693  
ID ADQ80368 standard; protein; 87 AA.  
DE FXD domain containing ion transport regulator 3 protein.  
PN WO2004063709-A2.  
PD 29-JUL-2004.  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
Query Match 46.5%; Score 214.5; DB 8; Length 87;  
Best Local Similarity 54.5%; Pred. No. 7.3e-19;  
RESULT 694  
ID ADZ69596 standard; protein; 87 AA.  
DE Human phospholemmann-like protein (PLML) SEQ ID NO:10.  
PN US2005101558-A1.  
PD 12-MAY-2005.  
PA (WATT/) WATT A T.  
Query Match 46.5%; Score 214.5; DB 9; Length 87;  
Best Local Similarity 54.5%; Pred. No. 7.3e-19;  
RESULT 695  
ID AEB29726 standard; protein; 87 AA.  
DE Human FXD domain-containing ion transport regulator 3.  
PN WO2005067667-A2.  
PD 28-JUL-2005.  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
Query Match 46.5%; Score 214.5; DB 9; Length 87;  
Best Local Similarity 54.5%; Pred. No. 7.3e-19;  
RESULT 696  
ID AED74451 standard; protein; 87 AA.  
DE Human placental protein SEQ ID NO:1279.  
PN US2005255114-A1.  
PD 17-NOV-2005.  
PA (NUVE-) NUVELO INC.  
Query Match 46.5%; Score 214.5; DB 9; Length 87;  
Best Local Similarity 54.5%; Pred. No. 7.3e-19;  
RESULT 697  
ID ABJ19334 standard; protein; 116 AA.  
DE NOVX related protein SEQ ID No 34.  
PN WO200299062-A2.  
PD 12-DEC-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 46.5%; Score 214.5; DB 6; Length 116;  
Best Local Similarity 54.5%; Pred. No. 1.1e-18;  
RESULT 698  
ID ADO41668 standard; protein; 116 AA.

Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 664  
ID ADM37965 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
FN US2004091959-A1.  
PD 13-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 8; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 665  
ID ADY77745 standard; protein; 89 AA.  
DE Neoplastic disease detection protein PRO1069.  
FN US200509102-A1.  
PD 17-MAR-2005.  
PA (EATO/) EATON D L.  
PA (FILV/) FILVAROFF E.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GRIM/) GRIMALDI J C.  
PA (GURN/) GURNEY A L.  
PA (WATA/) WATANABE C K.  
PA (WOOD/) WOOD W I.  
Query Match 100.0%; Score 461; DB 9; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 666  
ID AEA38515 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein, #143.  
FN US2005112725-A1.  
PD 26-MAY-2005.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 9; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 667  
ID AED50195 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
FN US2005163766-A1.  
PD 28-JUL-2005.  
Query Match 100.0%; Score 461; DB 9; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 668  
ID AEF12576 standard; protein; 89 AA.  
DE Human PRO1069 protein SEQ ID NO:50.  
FN US2006008901-A1.  
PD 12-JAN-2006.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 10; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 669  
ID AEF74265 standard; protein; 89 AA.  
DE Human PRO1069 protein SEQ ID NO:50.  
FN US2005260647-A1.  
PD 24-NOV-2005.  
PA (EATO/) EATON D L.  
PA (FILV/) FILVAROFF E.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GRIM/) GRIMALDI J C.  
PA (GURN/) GURNEY A L.  
PA (WATA/) WATANABE C K.  
PA (WOOD/) WOOD W L.  
Query Match 100.0%; Score 461; DB 10; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 670  
ID AAW92958 standard; protein; 89 AA.  
DE Human zsig44 protein.  
FN WO9905276-A1.  
PD 04-FEB-1999.  
PA (ZYMO ) ZYMOGENETICS INC.  
Query Match 98.0%; Score 452; DB 2; Length 89;  
Best Local Similarity 98.9%; Pred. No. 5.8e-49;  
RESULT 671

ID AAM38770 standard; protein; 89 AA.  
DE Human polypeptide SEQ ID NO 1915.  
FN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 98.0%; Score 452; DB 4; Length 89;  
Best Local Similarity 98.9%; Pred. No. 5.8e-49;  
RESULT 672  
ID ADK14984 standard; protein; 89 AA.  
DE Urinary specific protein #90.  
FN WO2003057839-A2.  
PD 17-JUL-2003.  
PA (DIAD-) DIADEXUS INC.  
Query Match 98.0%; Score 452; DB 7; Length 89;  
Best Local Similarity 98.9%; Pred. No. 5.8e-49;  
RESULT 673  
ID AAM40556 standard; protein; 117 AA.  
DE Human polypeptide SEQ ID NO 5487.  
FN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 98.0%; Score 452; DB 4; Length 117;  
Best Local Similarity 98.9%; Pred. No. 8.3e-49;  
RESULT 674  
ID ADP07847 standard; protein; 89 AA.  
DE Human secreted protein, seq id 330.  
FN WO2004042000-A2.  
PD 21-MAY-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 97.0%; Score 447; DB 8; Length 89;  
Best Local Similarity 97.8%; Pred. No. 2.5e-48;  
RESULT 675  
ID ADN38892 standard; protein; 186 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:210.  
FN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 81.1%; Score 374; DB 7; Length 186;  
Best Local Similarity 94.7%; Pred. No. 1.2e-38;  
RESULT 676  
ID ADN38894 standard; protein; 318 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:212.  
FN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 81.1%; Score 374; DB 7; Length 318;  
Best Local Similarity 94.7%; Pred. No. 2.3e-38;  
RESULT 677  
ID AAE05362 standard; protein; 88 AA.  
DE Mouse channel inducing factor precursor (CHIF) protein.  
FN WO200148192-A1.  
PD 05-JUL-2001.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
Query Match 60.0%; Score 276.5; DB 4; Length 88;  
Best Local Similarity 66.7%; Pred. No. 1e-26;  
RESULT 678  
ID ABE72374 standard; protein; 88 AA.  
DE Murine protein isolated from skin cells SEQ ID NO: 698.  
FN WO200190357-A1.  
PD 29-NOV-2001.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
Query Match 60.0%; Score 276.5; DB 5; Length 88;  
Best Local Similarity 66.7%; Pred. No. 1e-26;  
RESULT 679  
ID AAW92966 standard; protein; 87 AA.  
DE Rat CHIF protein.  
FN WO9905276-A1.  
PD 04-FEB-1999.  
PA (ZYMO ) ZYMOGENETICS INC.  
Query Match 55.6%; Score 256.5; DB 2; Length 87;  
Best Local Similarity 61.5%; Pred. No. 3.4e-24;  
RESULT 680  
ID AAR90991 standard; protein; 88 AA.

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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 646
ID ADH98932 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 647
ID ADI02162 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 648
ID ADH90701 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 649
ID ADJ54838 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 650
ID ADJ98576 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 651
ID ADJ98746 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 652
ID ADH78905 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 653
ID ADJ99139 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 654
ID ADJ99309 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 655
ID ADJ98927 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 656
ID ADH79075 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 657
ID ADX00935 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 658
ID ADK14456 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 659
ID ADJ64609 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 660
ID ADM31505 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 661
ID ADM36552 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 662
ID ADM40357 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 663
ID ADM80905 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
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DE Human secreted/transmembrane protein PRO1069.  
PN US200324358-A1.  
PD 04-DEC-2003.  
Query Match 100.0%; Score 461; DB 8; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 628  
ID ADH02207 standard; protein; 89 AA.  
DE Human PRO polypeptide #25.  
PN US2003180841-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 8; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 629  
ID ADG69211 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003180847-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 8; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 630  
ID ADG85996 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003180862-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 8; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 631  
ID ADH24932 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003180909-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 8; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 632  
ID ADH39549 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003180915-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 8; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 633  
ID ADH20041 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein PRO1069.  
PN US2003219856-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 8; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 634  
ID ADH02547 standard; protein; 89 AA.  
DE Human PRO polypeptide #25.  
PN US2003180840-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 8; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 635  
ID ADG69041 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003180849-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 8; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 636  
ID ADH07644 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003180850-A1.

PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 8; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 637  
ID ADG86166 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003180863-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 8; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 638  
ID ADH24762 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003180908-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 8; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 639  
ID ADH25810 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003180911-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 8; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 640  
ID ADH38376 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003180922-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 8; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 641  
ID ADH57215 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003181642-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 8; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 642  
ID ADH52203 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003180921-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 8; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 643  
ID ADH49569 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003180857-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 8; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 644  
ID ADH90531 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003181700-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 8; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 645  
ID ADI11267 standard; protein; 89 AA.  
DE Human PRO polypeptide #25.  
PN US2003181683-A1.  
PD 25-SEP-2003.

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RESULT 609
ID ADG69381 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 610
ID ADH39202 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 611
ID ADH26130 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 612
ID ADG83942 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 613
ID ADH19508 standard; protein; 89 AA.
DE Human secreted/transmembrane protein PRO1069.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 614
ID ADG85486 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 615
ID ADH06280 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 616
ID ADH30110 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 617
ID ADH24422 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 618
ID ADH21001 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 619
ID ADG69551 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 620
ID ADH07814 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 621
ID ADG85826 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 622
ID ADH39372 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 623
ID ADH33564 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 624
ID ADH33904 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 625
ID ADH01114 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 626
ID ADG69721 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 627
ID ADH21001 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 627
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RESULT 572  
ID ADI05414 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003190716-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 573  
ID ADH79486 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003191290-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 574  
ID ADI19443 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003181675-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 575  
ID ADI05244 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003181677-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 576  
ID ADH79656 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003191288-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 577  
ID ADI01482 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003181678-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 578  
ID ADI01652 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003181679-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 579  
ID ADI01822 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003181680-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 580  
ID ADH79826 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003191289-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 581  
ID ADI04644 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003171550-A1.  
PD 11-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 582  
ID ADI02780 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003181651-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 583  
ID ADH78099 standard; protein; 89 AA.  
DE Human PRO polypeptide #25.  
PN US2003181667-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 584  
ID ADI25738 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003181670-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 585  
ID ADI25908 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003181671-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 586  
ID ADK65420 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003073821-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 587  
ID ADH98762 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003191284-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 588  
ID ADH80003 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003191287-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 589  
ID ADL32806 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US200307396-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 590  
ID ADM30340 standard; protein; 89 AA.

Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 563  
ID ADI03080 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003181653-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 564  
ID ADH7929 standard; protein; 89 AA.  
DE Human PRO polypeptide #25.  
PN US2003181666-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 565  
ID ADH7912 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003181674-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 566  
ID ADI01297 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003190669-A1.  
PD 03-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 567  
ID ADI01992 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003181652-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 568  
ID ADI03250 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003181655-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 569  
ID ADI11437 standard; protein; 89 AA.  
DE Human PRO polypeptide #25.  
PN US2003181681-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 570  
ID ADI02339 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003181650-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 571  
ID ADI11777 standard; protein; 89 AA.  
DE Human PRO polypeptide #25.  
PN US2003181685-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;

DE Human secreted and transmembrane protein PRO1069.  
PN US2003181647-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 536  
ID ADH37965 standard; protein; 89 AA.  
DE Human secreted and transmembrane protein PRO1069.  
PN US2003181649-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 537  
ID ADH57385 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003180920-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 538  
ID ADH53527 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003181636-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 539  
ID ADH53697 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003181641-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 540  
ID ADH52033 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003181638-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 541  
ID ADH49888 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003181639-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 542  
ID ADI25398 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003181696-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 543  
ID ADH90191 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003181698-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 544  
ID ADI25568 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.

PN US2003181669-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 545  
ID ADH97742 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003181672-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 546  
ID ADI35443 standard; protein; 89 AA.  
DE Human PRO polypeptide #75.  
PN US2003050457-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 547  
ID ADI03590 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003181656-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 548  
ID ADI11947 standard; protein; 89 AA.  
DE Human PRO polypeptide #25.  
PN US2003181686-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 549  
ID ADH90021 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003181697-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 550  
ID ADH99935 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003049682-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 551  
ID ADH98422 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003181707-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 552  
ID ADI11097 standard; protein; 89 AA.  
DE Human PRO polypeptide #25.  
PN US2003181682-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 553  
ID ADI11607 standard; protein; 89 AA.  
DE Human PRO polypeptide #25.  
PN US2003181684-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.

Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 517  
ID ADF95229 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
FN US2003180795-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 518  
ID ADG12365 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
FN US2003207392-A1.  
PD 06-NOV-2003.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 519  
ID ADH24082 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
FN US2003180918-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 520  
ID ADH34108 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
FN US2003180858-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 521  
ID ADH29941 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
FN US2003180859-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 522  
ID ADH23912 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
FN US2003180919-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 523  
ID ADH09025 standard; protein; 89 AA.  
DE Human PRO polypeptide #100.  
FN US2003207395-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 524  
ID ADG85316 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
FN US2003180904-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 525  
ID ADH24592 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
FN US2003180907-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 526  
ID ADH37788 standard; protein; 89 AA.  
DE Human secreted and transmembrane protein PRO1069.  
FN US2003181646-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 527  
ID ADH02037 standard; protein; 89 AA.  
DE Human PRO polypeptide #25.  
FN US2003180837-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 528  
ID ADH37618 standard; protein; 89 AA.  
DE Human secreted and transmembrane protein PRO1069.  
FN US2003181648-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 529  
ID ADG85656 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
FN US2003180905-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 530  
ID ADH24252 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
FN US2003180914-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 531  
ID ADH38546 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
FN US2003181643-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 532  
ID ADG83667 standard; protein; 89 AA.  
DE Human PRO polypeptide #25.  
FN US2003180794-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 533  
ID ADH29475 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
FN US2003180860-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 534  
ID ADH27591 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
FN US2003180906-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 535  
ID ADH37788 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
FN US2003180906-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 536  
ID ADH37788 standard; protein; 89 AA.

PD 10-APR-2003.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 498  
ID ADC81919 standard; protein; 89 AA.  
DE Human PRO polypeptide #75.  
PN US2003083461-A1.  
PD 01-MAY-2003.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 499  
ID ADD07561 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2002193299-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 500  
ID ADC82452 standard; protein; 89 AA.  
DE Human PRO polypeptide #75.  
PN US2003059833-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 501  
ID ADD05673 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003087376-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 502  
ID ADD08632 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003073050-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 503  
ID ADD06881 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2002193300-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 504  
ID ADC83128 standard; protein; 89 AA.  
DE Human PRO polypeptide #75.  
PN US2003059783-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 505  
ID ADD55235 standard; protein; 89 AA.  
DE Human PRO polypeptide #75.  
PN US2003077593-A1.  
PD 24-APR-2003.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 506  
ID ADD36054 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003105298-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 507  
ID ADD56193 standard; protein; 89 AA.  
DE Human PRO polypeptide #75.

PN US2003077594-A1.  
PD 24-APR-2003.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 508  
ID ADD54631 standard; protein; 89 AA.  
DE Human PRO polypeptide #75.  
PN US2002132253-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 509  
ID ADE26785 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003087304-A1.  
PD 08-MAY-2003.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 510  
ID ADE26252 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003087305-A1.  
PD 08-MAY-2003.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 511  
ID ADF67189 standard; protein; 89 AA.  
DE Human PRO1069 amino acid sequence SEQ ID NO:262.  
PN US2002198148-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 512  
ID ADG01055 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003078387-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 513  
ID ADG08608 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003180793-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 514  
ID ADG02668 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003207397-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 515  
ID ADG01375 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003207399-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 516  
ID ADF95550 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003207398-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;

[illegible]

Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 460  
ID ABO37416 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003068726-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 461  
ID ABO28214 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003064459-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 462  
ID ABO22995 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003068757-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 463  
ID ABO30315 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003068723-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 464  
ID ABO21775 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003068741-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 465  
ID ABO21470 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003068744-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 466  
ID ABO15001 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003068766-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 467  
ID ABO41076 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003068694-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 468  
ID ABO36806 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003068715-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 469  
ID ABO37416 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003068726-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 470  
ID ABO75206 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003104544-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 471  
ID ABO33486 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003096357-A1.  
PD 22-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 472  
ID ABO46241 standard; protein; 89 AA.  
DE Human PRO polypeptide #100.  
PN US2003049760-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 473  
ID ADA82635 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003049755-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 474  
ID ADB85623 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003049735-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 475  
ID ADB96270 standard; protein; 89 AA.  
DE Human PRO polypeptide #75.  
PN US2003054403-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 476  
ID ABO31840 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003068680-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 477  
ID ABO31230 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003068762-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 478  
ID ADB85943 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.

PN	US2003064442-A1.	Query Match	100.0%;	Score 461;	DB 7;	Length 89;
PD	03-APR-2003.	Best Local Similarity	100.0%;	Pred. No. 4.2e-50;		
PA	( GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 461;	DB 7;	Length 89;		
Best Local Similarity	100.0%;	Pred. No. 4.2e-50;				
RESULT 441						
ID	ABM13171 standard; protein; 89 AA.					
DE	Human secreted polypeptide PRO1069, SEQ ID NO:200.					
PN	US2003064450-A1.					
PD	03-APR-2003.					
PA	( GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 461;	DB 7;	Length 89;		
Best Local Similarity	100.0%;	Pred. No. 4.2e-50;				
RESULT 442						
ID	ABO11874 standard; protein; 89 AA.					
DE	Human secreted/transmembrane protein (PRO) #100.					
PN	US2003068731-A1.					
PD	10-APR-2003.					
PA	( GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 461;	DB 7;	Length 89;		
Best Local Similarity	100.0%;	Pred. No. 4.2e-50;				
RESULT 443						
ID	ABM14086 standard; protein; 89 AA.					
DE	Human secreted polypeptide PRO1069, SEQ ID NO:200.					
PN	US2003068683-A1.					
PD	10-APR-2003.					
PA	( GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 461;	DB 7;	Length 89;		
Best Local Similarity	100.0%;	Pred. No. 4.2e-50;				
RESULT 444						
ID	ABM08291 standard; protein; 89 AA.					
DE	Human secreted polypeptide PRO1069, SEQ ID NO:200.					
PN	US2003068754-A1.					
PD	10-APR-2003.					
PA	( GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 461;	DB 7;	Length 89;		
Best Local Similarity	100.0%;	Pred. No. 4.2e-50;				
RESULT 445						
ID	ABO40161 standard; protein; 89 AA.					
DE	Human secreted/transmembrane protein (PRO) #100.					
PN	US2003068681-A1.					
PD	10-APR-2003.					
PA	( GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 461;	DB 7;	Length 89;		
Best Local Similarity	100.0%;	Pred. No. 4.2e-50;				
RESULT 446						
ID	ABM74596 standard; protein; 89 AA.					
DE	Human secreted polypeptide PRO1069, SEQ ID NO:200.					
PN	US2003096351-A1.					
PD	22-MAY-2003.					
PA	( GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 461;	DB 7;	Length 89;		
Best Local Similarity	100.0%;	Pred. No. 4.2e-50;				
RESULT 447						
ID	ABM33791 standard; protein; 89 AA.					
DE	Human secreted polypeptide PRO1069, SEQ ID NO:200.					
PN	US2003096358-A1.					
PD	22-MAY-2003.					
PA	( GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 461;	DB 7;	Length 89;		
Best Local Similarity	100.0%;	Pred. No. 4.2e-50;				
RESULT 448						
ID	ABM20250 standard; protein; 89 AA.					
DE	Human secreted polypeptide PRO1069, SEQ ID NO:200.					
PN	US2003104556-A1.					
PD	05-JUN-2003.					
PA	( GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 461;	DB 7;	Length 89;		
Best Local Similarity	100.0%;	Pred. No. 4.2e-50;				
RESULT 449						
ID	ABO48742 standard; protein; 89 AA.					
DE	Human secreted/transmembrane protein (PRO) #100.					
PN	US2003049756-A1.					
PD	13-MAR-2003.					
PA	( GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 461;	DB 7;	Length 89;		
Best Local Similarity	100.0%;	Pred. No. 4.2e-50;				
RESULT 450						
ID	ABO22550 standard; protein; 89 AA.					
DE	Human secreted/transmembrane protein PRO1069.					
PN						



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DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
  100.0%; Score 461; DB 7; Length 89;
Best Local Similarity
  100.0%; Pred. No. 4.2e-50;
RESULT 422
ID ABO29434 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
  100.0%; Score 461; DB 7; Length 89;
Best Local Similarity
  100.0%; Pred. No. 4.2e-50;
RESULT 423
ID ABO31264 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
  100.0%; Score 461; DB 7; Length 89;
Best Local Similarity
  100.0%; Pred. No. 4.2e-50;
RESULT 424
ID ABM14391 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
  100.0%; Score 461; DB 7; Length 89;
Best Local Similarity
  100.0%; Pred. No. 4.2e-50;
RESULT 425
ID ABM09816 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
  100.0%; Score 461; DB 7; Length 89;
Best Local Similarity
  100.0%; Pred. No. 4.2e-50;
RESULT 426
ID ABO38941 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
  100.0%; Score 461; DB 7; Length 89;
Best Local Similarity
  100.0%; Pred. No. 4.2e-50;
RESULT 427
ID ABM34706 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003104538-A1.
PD 05-JUN-2003.
Query Match
  100.0%; Score 461; DB 7; Length 89;
Best Local Similarity
  100.0%; Pred. No. 4.2e-50;
RESULT 428
ID ABO51182 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
  100.0%; Score 461; DB 7; Length 89;
Best Local Similarity
  100.0%; Pred. No. 4.2e-50;
RESULT 429
ID ABO04008 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003036158-A1.
PD 20-FEB-2003.
Query Match
  100.0%; Score 461; DB 7; Length 89;
Best Local Similarity
  100.0%; Pred. No. 4.2e-50;
RESULT 430
ID ABO10478 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003036151-A1.
PD 20-FEB-2003.
Query Match
  100.0%; Score 461; DB 7; Length 89;
Best Local Similarity
  100.0%; Pred. No. 4.2e-50;
RESULT 431
ID ABO53180 standard; protein; 89 AA.
DE Human secreted/transmembrane protein PRO1069.
PN US2003044806-A1.
PD 06-MAR-2003.
Query Match
  100.0%; Score 461; DB 7; Length 89;
Best Local Similarity
  100.0%; Pred. No. 4.2e-50;
RESULT 432
ID ABR77721 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003040067-A1.
PD 27-FEB-2003.
Query Match
  100.0%; Score 461; DB 7; Length 89;
Best Local Similarity
  100.0%; Pred. No. 4.2e-50;
RESULT 433
ID ABR78931 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003054456-A1.
PD 20-MAR-2003.
Query Match
  100.0%; Score 461; DB 7; Length 89;
Best Local Similarity
  100.0%; Pred. No. 4.2e-50;
RESULT 434
ID ABO24025 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
  100.0%; Score 461; DB 7; Length 89;
Best Local Similarity
  100.0%; Pred. No. 4.2e-50;
RESULT 435
ID ABR93789 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
  100.0%; Score 461; DB 7; Length 89;
Best Local Similarity
  100.0%; Pred. No. 4.2e-50;
RESULT 436
ID ABM01832 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
  100.0%; Score 461; DB 7; Length 89;
Best Local Similarity
  100.0%; Pred. No. 4.2e-50;
RESULT 437
ID ABM78255 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
  100.0%; Score 461; DB 7; Length 89;
Best Local Similarity
  100.0%; Pred. No. 4.2e-50;
RESULT 438
ID ABR90044 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
  100.0%; Score 461; DB 7; Length 89;
Best Local Similarity
  100.0%; Pred. No. 4.2e-50;
RESULT 439
ID ADA22385 standard; protein; 89 AA.
DE Human secreted/transmembrane polypeptide PRO1069.
PN US2003040473-A1.
PD 27-FEB-2003.
Query Match
  100.0%; Score 461; DB 7; Length 89;
Best Local Similarity
  100.0%; Pred. No. 4.2e-50;
RESULT 440
ID ABM27570 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
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PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 384
ID ADA00381 standard; protein; 89 AA.
DE Human secreted/transmembrane polypeptide PRO 1069.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 385
ID ABM26960 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 386
ID ABM03357 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 387
ID ABO39856 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 388
ID ABO49962 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 389
ID ABO50877 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 390
ID ABO5333 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003036126-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 391
ID ABR74637 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003044924-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 392
ID ABR77116 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003044927-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 393
ID ABM17873 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003040072-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 394
ID ABR95924 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003040073-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 395
ID ABO21857 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 396
ID ABO20027 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003032124-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 397
ID ABO24330 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 398
ID ABR86079 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 399
ID ABM10731 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 400
ID ABM76730 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 401
ID ABR89434 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003073170-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 402
ID ABM12561 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003073176-A1.
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RESULT 365  
ID ABM11341 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
FN US2003064469-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 366  
ID ABO32948 standard; protein; 89 AA.  
DE Human PRO polypeptide #100.  
FN US2003064453-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 367  
ID ABO30654 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
FN US2003064466-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 368  
ID ABO30959 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
FN US2003064468-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 369  
ID ABM27265 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
FN US2003068760-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 370  
ID ABM30010 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
FN US2003068769-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 371  
ID ABM05546 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
FN US2003068698-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 372  
ID ABM15611 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
FN US2003068698-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 373  
ID ABM08596 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
FN US2003068759-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 374  
ID ABR88214 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
FN US2003068759-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 375  
ID ABO38026 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
FN US2003068765-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 376  
ID ABO45936 standard; protein; 89 AA.  
DE Human PRO polypeptide #100.  
FN US2003049754-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 377  
ID ABM66739 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
FN US2003068688-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 378  
ID ADB20312 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
FN US2003082767-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 379  
ID ABM19640 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
FN US2003104552-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 380  
ID ABO49352 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
FN US2003049774-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 381  
ID ABO49657 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
FN US2003049775-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 382  
ID ADA78564 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
FN US2003073181-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 383  
ID ABR88214 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
FN US2003073181-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;

PN US2003104541-A1.  
PD 05-JUN-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 346  
ID ABM19945 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003104554-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 347  
ID ABO46851 standard; protein; 89 AA.  
DE Human PRO polypeptide #100.  
PN US2003049762-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 348  
ID ABO47156 standard; protein; 89 AA.  
DE Human PRO polypeptide #100.  
PN US2003049765-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 349  
ID ADA83269 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003049752-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 350  
ID ABR71587 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003032133-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 351  
ID ABR72197 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003032136-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 352  
ID ABR98836 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003036129-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 353  
ID ABO06906 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003040053-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 354  
ID ABR84859 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003040057-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 355  
ID ABR73417 standard; protein; 89 AA.

DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003054467-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 356  
ID ABR76511 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003044932-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 357  
ID ABR73112 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003027270-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 358  
ID ABM18178 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003054469-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 359  
ID ABO20637 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003032126-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 360  
ID ABO25380 standard; protein; 89 AA.  
DE Human PRO polypeptide #100.  
PN US2003054463-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 361  
ID ABO25685 standard; protein; 89 AA.  
DE Human PRO polypeptide #100.  
PN US2003054466-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 362  
ID ABR94094 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003059879-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 363  
ID ADA92824 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein PRO1069.  
PN US2003060407-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 364  
ID ABR80001 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003049738-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;

PN US2003049750-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 327  
ID AB051487 standard; protein; 89 AA.  
DE Human PRO polypeptide #100.  
PN US2003049766-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 328  
ID AB051792 standard; protein; 89 AA.  
DE Human PRO polypeptide #100.  
PN US2003049767-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 329  
ID AB050572 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003049779-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 330  
ID ABR79696 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003040059-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 331  
ID ABM16958 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003040078-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 332  
ID ABO17990 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003044918-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 333  
ID ABO20942 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003032132-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 334  
ID ABR96901 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003054462-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 335  
ID ADA38703 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein PRO1069.  
PN US2003059780-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;

RESULT 336  
ID ABM12256 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003064445-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 337  
ID ABM16348 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003064449-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 338  
ID ABM24215 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003064441-A1.  
PD 03-APR-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 339  
ID ABM14696 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003068696-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 340  
ID ABO4577 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003068712-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 341  
ID ABO6766 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003068730-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 342  
ID ABO9206 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003073174-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 343  
ID ABO39246 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003068775-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 344  
ID ABM75511 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003104545-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 345  
ID ABM25435 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.

PD 06-MAR-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 308  
ID ABO22722 standard; protein; 89 AA.  
DE Human secreted polypeptide #100.  
PN US2003027265-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 309  
ID ABO23027 standard; protein; 89 AA.  
DE Human secreted polypeptide #100.  
PN US2003054461-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 310  
ID ABR92569 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003064446-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 311  
ID ABR81526 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003049744-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 312  
ID ABR77950 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003049783-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 313  
ID ABR89739 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003073171-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 314  
ID ABM26655 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003032121-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 315  
ID ABM13781 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003064458-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 316  
ID ABO28519 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003064460-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 317  
ID ABO30349 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003064464-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 318  
ID ABM07376 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003068702-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 319  
ID ABM03967 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003068734-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 320  
ID ABO37111 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003068719-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 321  
ID ABO41686 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003068729-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 322  
ID ABO35281 standard; protein; 89 AA.  
DE Human secreted polypeptide #100.  
PN US2003068738-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 323  
ID ABM25130 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003104540-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 324  
ID ABO47522 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003049742-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 325  
ID ABO47827 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003049747-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 326  
ID ABO48437 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.

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PD 13-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 289
ID ABO211247 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003054454-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 290
ID ABO22162 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003054477-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 291
ID ADA20084 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003055222-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 292
ID ABO34191 standard; protein; 89 AA.
DE Human secreted/transmembrane polypeptide PRO 1069.
PN US2003060601-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 293
ID ABR96596 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003054460-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 294
ID ADA94478 standard; protein; 89 AA.
DE Human secreted/transmembrane protein PRO1069.
PN US2003059832-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 295
ID ABR85774 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003049753-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 296
ID ABR99756 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003049763-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 297
ID ABR99756 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003049763-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 298
ID ABR99756 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003049763-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 299
ID ABO29739 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068700-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 300
ID ABO29739 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068700-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 301
ID ABO29739 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068700-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 302
ID ABO38331 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068767-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 303
ID ABO45631 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003073182-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 304
ID ABO45631 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003104557-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 305
ID ADA81471 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003092121-A1.
PD 15-MAY-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 306
ID ABO16669 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003027276-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 307
ID ABO18295 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US200304920-A1.
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Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 270
ID ADA79744 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003073173-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 271
ID ABR96291 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003054458-A1.
PD 20-NAR-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 272
ID ABR96291 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003054458-A1.
PD 20-NAR-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 273
ID ABR96384 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003049758-A1.
PD 13-NAR-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 274
ID ABR86689 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003049772-A1.
PD 13-NAR-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 275
ID ABR16653 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003064448-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 276
ID ABR29705 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003064456-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 277
ID ABO29129 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068693-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 278
ID ABR23910 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068735-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 279
ID ABO20332 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003032125-A1.
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ID ABM23300 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068753-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 280
ID ABM22080 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068742-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 281
ID ABO37721 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068756-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 282
ID ABM28485 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003082715-A1.
PD 01-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 283
ID ABM28730 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003082716-A1.
PD 01-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 284
ID ABM66434 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068737-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 285
ID ABM75816 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003104547-A1.
PD 05-JUN-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 286
ID ABM34096 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003096359-A1.
PD 22-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 287
ID ABM34401 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003100061-A1.
PD 29-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 288
ID ABO20332 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003032125-A1.
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PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 251  
ID AB050267 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US20030409777-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 252  
ID AB099261 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003040055-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 253  
ID AB004313 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003036164-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 254  
ID AB005943 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003040074-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 255  
ID ABM18483 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003054480-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 256  
ID ADA27898 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein PRO1069.  
PN US2003054359-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 257  
ID ABR97511 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003059885-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 258  
ID ABR80611 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003049740-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 259  
ID ABM01222 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003049770-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 260  
ID ABR88824 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003096353-A1.  
PD 22-MAY-2003.

DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003073169-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 261  
ID ABM13476 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003064457-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 262  
ID ABM20860 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003068711-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 263  
ID ABO41991 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003049745-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 264  
ID ABO42601 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003049751-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 265  
ID ABM10121 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003067478-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 266  
ID ABO38636 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003068773-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 267  
ID ABM32876 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003073185-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 268  
ID ABM22690 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003087373-A1.  
PD 08-MAY-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 269  
ID ABM74901 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003096353-A1.  
PD 22-MAY-2003.

RESULT 232  
ID ABO52402 standard; protein; 89 AA.  
DE Human PRO polypeptide #100.  
PN US2003049771-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 233  
ID ADA11912 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003069394-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 234  
ID ABO231720 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003032134-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 235  
ID ADB17295 standard; protein; 89 AA.  
DE Human transmembrane PRO polypeptide (SeqID 50).  
PN US2003050465-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 236  
ID ADA17790 standard; protein; 89 AA.  
DE Human PRO1069 polypeptide.  
PN US2003054987-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 237  
ID ABR97206 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003054481-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 238  
ID ABR86994 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003049778-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 239  
ID ABM11036 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003049782-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 240  
ID ABM28180 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003054476-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 241  
ID ABO32179 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003049773-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 242  
ID ABM15306 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003068692-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 243  
ID ABM06461 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003068709-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 244  
ID ABM04272 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003068716-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 245  
ID ABM22385 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003068740-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 246  
ID ABM07681 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003068751-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 247  
ID ABO40771 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003068684-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 248  
ID ABM35418 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003073179-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 249  
ID ABM33181 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003087374-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 250  
ID ABO52707 standard; protein; 89 AA.  
DE Human PRO polypeptide #100.  
PN US2003049773-A1.  
PD 13-MAR-2003.

PN US2003054470-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 214  
ID ABR94399 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003044917-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 215  
ID ABR75906 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003044929-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 216  
ID ABR71282 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003059880-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 217  
ID ABR931179 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003064465-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 218  
ID ABR93484 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003054478-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 219  
ID ADA10246 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein, PRO1069.  
PN US2003059831-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 220  
ID ABR87909 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003068718-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 221  
ID ABO27909 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003064454-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 222  
ID ABO30044 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003064461-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 223  
ID ABO33553 standard; protein; 89 AA.  
DE Human PRO polypeptide #100.  
PN US2003068724-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 224  
ID ABO4941 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003068727-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 225  
ID ABO8901 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003068772-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 226  
ID ABO36501 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003068714-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 227  
ID ABO35586 standard; protein; 89 AA.  
DE Human PRO polypeptide #100.  
PN US2003068758-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 228  
ID ABO39551 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003068776-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 229  
ID ABO10426 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003069407-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 230  
ID ABO11951 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003104555-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 231  
ID ABO52097 standard; protein; 89 AA.  
DE Human PRO polypeptide #100.  
PN US2003049768-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;

DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003064463-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 195  
ID ABO27604 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003064451-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 196  
ID ABM29095 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003068721-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 197  
ID ABM07071 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003068699-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 198  
ID ABM21165 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003068707-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 199  
ID ABM09511 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003073175-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 200  
ID ABO41381 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003068695-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 201  
ID ABO36196 standard; protein; 89 AA.  
DE Human PRO polypeptide #100.  
PN US2003068703-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 202  
ID ABO43725 standard; protein; 89 AA.  
DE Human PRO polypeptide #100.  
PN US2003068732-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 203  
ID ABM76425 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003082717-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 204  
ID ABM76121 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003104548-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 205  
ID ABM25740 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003104542-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 206  
ID ABM26045 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003104543-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 207  
ID ADA21459 standard; protein; 89 AA.  
DE Human secreted/transmembrane polypeptide PRO1069.  
PN US2003054404-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 208  
ID ABO03398 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003036127-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 209  
ID ABO02483 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003040061-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 210  
ID ABO44263 standard; protein; 89 AA.  
DE Human secreted/transmembrane polypeptide PRO 1069.  
PN US2003018172-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 211  
ID ABR90654 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003036130-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 212  
ID ABR73722 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003054468-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 213  
ID ABO16974 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.

ID AEW03662 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003068722-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 186  
ID ADM35113 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003073183-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 187  
ID ARM26350 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003104549-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 188  
ID ASO48132 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003049749-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 189  
ID APR92874 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003064462-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 190  
ID ASO24635 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003065159-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 191  
ID ADA37773 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein PRO1069.  
PN US2003008297-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 192  
ID AWL1646 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003064447-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 193  
ID ABM02747 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003073184-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 194  
ID ABM16043 standard; protein; 89 AA.

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Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 157
ID ABO05638 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 158
ID ABR74027 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 159
ID ABR95619 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 160
ID ABR80916 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 161
ID ABR81221 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 162
ID ABM00917 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 163
ID ABR88519 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 164
ID ABM77340 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 165
ID ABO28824 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 166
ID ABO31569 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 167
ID ABM07986 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 168
ID ABO40466 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 169
ID ABO35891 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 170
ID ABO44030 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 171
ID ADA77952 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 172
ID ABM24825 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003104539-A1.
PD 05-JUN-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 173
ID ABO03093 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003036131-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 174
ID ABR90349 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 175
ID ABM17263 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
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DE Human secreted/transmembrane protein (PRO) #100.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 138
ID ABR69757 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 139
ID ABU80134 standard; protein; 89 AA.
DE Human PRO protein #100.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 140
ID ABU82499 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 141
ID ABU92183 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 142
ID ABU93403 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 143
ID ABO09956 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 144
ID ABO09041 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 145
ID ABU96463 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 146
ID ABU10889 standard; protein; 89 AA.
DE Human PRO polypeptide #75.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 147
ID ABU10609 standard; protein; 89 AA.
DE Human secreted/transmembrane protein #100.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 148
ID ABU81641 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 149
ID ABU72133 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 150
ID ABU95618 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 151
ID ABU96827 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 152
ID ABR70672 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 153
ID ABO05023 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 154
ID ABO08431 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 155
ID ABU8580 standard; protein; 89 AA.
DE Human secreted and transmembrane polypeptide PRO1069.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 156
ID ABO34094 standard; protein; 89 AA.
DE Human PRO1069 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
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Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 117  
ID ABU94691 standard; protein; 89 AA.  
DE Human PRO polypeptide #100.  
PN US2003032103-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 118  
ID ABO04618 standard; protein; 89 AA.  
DE Human PRO polypeptide #100.  
PN US2003032107-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 119  
ID ABR70367 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003032139-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 120  
ID ABU92352 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003022187-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 121  
ID ABU98532 standard; protein; 89 AA.  
DE Human PRO polypeptide #100.  
PN US2003022301-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 122  
ID ABR65931 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003036165-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 123  
ID ABR64648 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003027262-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 124  
ID ABU59417 standard; protein; 89 AA.  
DE Novel human secreted or transmembrane protein PRO1129.  
PN US2003027985-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 125  
ID ABU79573 standard; protein; 89 AA.  
DE Human PRO polypeptide #100.  
PN US2003032110-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 126  
ID ABU92964 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003036142-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 127

Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 128  
ID ABU91143 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003036154-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 129  
ID ABU90236 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003036153-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 130  
ID ABO09651 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003044931-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 131  
ID ABO10923 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003036150-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 132  
ID ABR70977 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003040069-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 133  
ID ABU98287 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2002183493-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 134  
ID ABU87585 standard; protein; 89 AA.  
DE Human PRO polypeptide #100.  
PN US2003022293-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 135  
ID ABU91453 standard; protein; 89 AA.  
DE Human PRO polypeptide #100.  
PN US2003032128-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 136  
ID ABU89292 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003036634-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 137  
ID ABU84667 standard; protein; 89 AA.

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Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 97
ID ABU85982 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
FN US2003022300-A1.
PD 30-JAN-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 98
ID ABU82269 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
FN US2003036136-A1.
PD 20-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 99
ID ABU87280 standard; protein; 89 AA.
DE Human secreted polypeptide #100.
FN US2003036138-A1.
PD 20-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 100
ID ABU83752 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
FN US2003032109-A1.
PD 13-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 101
ID AB008126 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
FN US2003040066-A1.
PD 27-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 102
ID ABU92500 standard; protein; 89 AA.
DE Human secreted/transmembrane protein PRO1069.
FN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 103
ID ABU81837 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
FN US2003032104-A1.
PD 13-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 104
ID ABU66001 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
FN US2003036157-A1.
PD 20-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 105
ID ABU81170 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069.
FN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 106
ID ABR59830 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
FN US2003032120-A1.
PD 13-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;

Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 107
ID ABU94018 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
FN US2003036155-A1.
PD 20-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 108
ID ABU99871 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
FN US2003022296-A1.
PD 30-JAN-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 109
ID ABR66541 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
FN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 110
ID ABR90959 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
FN US2003040058-A1.
PD 27-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 111
ID ABO53285 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
FN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 112
ID ABU58974 standard; protein; 89 AA.
DE Human secreted/transmembrane protein, #105.
FN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 113
ID ABU94386 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
FN US2003017540-A1.
PD 23-JAN-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 114
ID ABU79268 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
FN US2003032106-A1.
PD 13-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 115
ID ABU86597 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
FN US2003032129-A1.
PD 13-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 116
ID ABU86902 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
FN US2003032131-A1.
PD 13-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
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PD 13-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 77
ID ABUS0984 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003018458-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 78
ID ABR67870 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 79
ID ABR65258 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 80
ID ABR68480 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 81
ID ABR71892 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US200302135-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 82
ID ABUS9268 standard; protein; 89 AA.
DE Human secreted/transmembrane protein, #105.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 83
ID ABUS5372 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 84
ID ABUS9062 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 85
ID ABUS3142 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 86
ID ABUS4998 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 87
ID ABUS0546 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 88
ID ABUS4057 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 89
ID ABUS3708 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003032119-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 90
ID ABUS25965 standard; protein; 89 AA.
DE Human PRO1069 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 91
ID ABR64953 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 92
ID ABO27305 standard; protein; 89 AA.
DE Human secreted/transmembrane polypeptide PRO1069.
PN US2003009012-A1.
PD 09-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 93
ID ABR68785 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 94
ID ABO06601 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 95
ID ABR99146 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 96
ID ABUS7030 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003027280-A1.
PD 06-FEB-2003.
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PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 57
ID ABR66846 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 58
ID AB016059 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 59
ID AB013765 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 60
ID AB071530 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 61
ID AB065668 standard; protein; 89 AA.
DE Human secreted/transmembrane protein, SEQ ID 200.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 62
ID AB007516 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 63
ID AB003703 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 64
ID ABR67151 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 65
ID AB015754 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 66
ID AB056035 standard; protein; 89 AA.
DE Human secreted/transmembrane protein, PRO1069.
PN US2003022298-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 67
ID AB072311 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 68
ID AB065363 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 69
ID AB095308 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 70
ID AB071211 standard; protein; 89 AA.
DE Human PRO1069 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 71
ID AB007821 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 72
ID ABR70062 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 73
ID ABR69395 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 74
ID AB001536 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 75
ID AB081338 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 76
ID ABR60135 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003032137-A1.
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PN US2003003531-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 37  
ID ABU90900 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003018173-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 38  
ID ABO33959 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein PRO1069.  
PN US2003009013-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 39  
ID ABR99451 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003040063-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 40  
ID ABR98841 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003040064-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 41  
ID ABO16364 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003027267-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 42  
ID ABR92264 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003036160-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 43  
ID ABO18905 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003044925-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 44  
ID ABR78326 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003054474-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 45  
ID ABU71976 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003018183-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 46

ID ABU85062 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003032114-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 47  
ID ABO00201 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003032101-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 48  
ID ABO11533 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003036124-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 49  
ID ABO02178 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003040054-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 50  
ID ABU88752 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003036133-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 51  
ID ABU83447 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003036134-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 52  
ID ABO06248 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003022294-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 53  
ID ABR59284 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003027275-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 54  
ID ABO09346 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003027324-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 55  
ID ABO19210 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003036118-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 56  
ID ABO11228 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.

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PN US2003032023-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 17
ID ABU13934 standard; protein; 89 AA.
DE Human PRO1069 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH ) GENENTECH LTD.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 28
ID ABU85677 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 29
ID ABU98837 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 30
ID ABU98052 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 31
ID ABU91758 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 32
ID ABU89451 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 33
ID ABU86292 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 34
ID ABU67505 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 35
ID ABU80533 standard; protein; 89 AA.
DE Human PRO protein #100.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 36
ID ABU72519 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003032023-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 17
ID ABU82805 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 18
ID ABU89926 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 19
ID ABR68175 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 20
ID ABU60552 standard; protein; 89 AA.
DE Human secreted/transmembrane protein, #105.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 21
ID ABU96228 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 22
ID ABU92659 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 23
ID AB008736 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 24
ID AB002788 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 25
ID ABR74942 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 26
ID ABR94704 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003044926-A1.
PD 06-MAR-2003.
```

OM protein - protein search, using sw model  
Run on: November 21, 2006, 19:47:43 ; Search time 201 Seconds.  
(without alignments)  
202.449 Million cell updates/sec

Title: US-10-063-557-50  
Perfect score: 461  
Sequence: 1 MERVTLALLLAGLTALEAN.....HSPVPEKAIPITPGSATTC 89  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Total number of hits satisfying chosen parameters: 2589679  
Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database : A\_Geneseq 8:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	AA66705	standard; protein; 89 AA.				
DE	Membrane-bound protein PRO1069.					
PN	WO9963088-A2.					
PD	09-DEC-1999.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 461;	DB 3;	Length 89;		
Best Local Similarity	100.0%;	Pred. No. 4.2e-50;				
RESULT 2						
ID	AA87258	standard; protein; 89 AA.				
DE	Human signal peptide containing protein HSP-35					
PN	WO20000610-A2.					
PD	06-JAN-2000.					
PA	(INCY-) INCYTE PHARM INC.					
Query Match	100.0%;	Score 461;	DB 3;	Length 89;		
Best Local Similarity	100.0%;	Pred. No. 4.2e-50;				
RESULT 3						
ID	RAY85679	standard; protein; 89 AA.				
DE	Human kidney disease associated protein SEQ ID 11.					
PN	WO200061622-A2.					
PD	19-OCT-2000.					
PA	(INCY-) INCYTE PHARM INC.					
Query Match	100.0%;	Score 461;	DB 3;	Length 89;		
Best Local Similarity	100.0%;	Pred. No. 4.2e-50;				
RESULT 4						
ID	AAU29123	standard; protein; 89 AA.				
DE	Human PRO polypeptide sequence #100.					
PN	WO200168848-A2.					
PD	20-SEP-2001.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 461;	DB 3;	Length 89;		
Best Local Similarity	100.0%;	Pred. No. 4.2e-50;				
RESULT 5						
ID	AAB87550	standard; protein; 89 AA.				
DE	Human PRO1069.					
PN	WO200116318-A2.					
PD	08-MAR-2001.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 461;	DB 4;	Length 89;		
Best Local Similarity	100.0%;	Pred. No. 4.2e-50;				
RESULT 6						
ID	AAB65228	standard; protein; 89 AA.				
DE	Human PRO1069 (UNQ526) protein sequence SEQ ID NO:262.					

PN WO200073454-A1.  
PD 07-DEC-2000.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 4; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 7  
ID ABG95875 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein PRO1069.  
PN US2002119130-A1.  
PD 29-AUG-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 5; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 8  
ID ABU58499 standard; protein; 89 AA.  
DE Human PRO polypeptide #100.  
PN US2003027272-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 9  
ID ABU88047 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003032127-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 10  
ID ABU84362 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003032112-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 11  
ID ABR66236 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003027278-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 12  
ID ABR65626 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003036159-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 13  
ID ABU99566 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003040070-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 14  
ID ABUS8043 standard; protein; 89 AA.  
DE Human PRO polypeptide #75.  
PN US2003027163-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 15  
ID ABUS9121 standard; protein; 89 AA.  
DE Novel human secreted or transmembrane protein PRO1069.  
PN US2002132252-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.2e-50;  
RESULT 16  
ID ABU82633 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein PRO1069.